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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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88. .140 - _ _ /label= active_site_aspartic_acid_region

/label= potential_phosphorylation_site 102 /label= potential_phosphorylation_site

99WO-US025021. 98US-00181317. 99US-00234726.

label= potential_glycosylation_site

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07-DEC-1999;

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Human phospholipase genes and proteins useful to diagnose, prevent treat cancer, autoimmune or inflammatory or reproductive disorders.
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                                                                          Claim 1; Page 70-71; 80pp; English.
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Best Local Similarity 100.
Matches 145; Conservative
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tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
                                                                                                                                                                                                                                                                                                                                                     The present invention describes human secretory phospholipase A2 (PLA2). PLA2 has antiallergic, antiinflammatory, antibacterial, tranquillser, immunosuppressive, vulnerary, antirheumatic and antiarthritic activities. Human secretory phospholipase A2 (PLA2), the gene encoding it and antibodies against it are useful for the diagnosis and treatment of secretory PLA2-associated diseases e.g. septic shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The
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                                                                                                                                                                                                           Human secretory phospholipase A2 (PLA2) and its encoded gene for diagnosis and treatment of secretory PLA2-associated diseases e.g. seg shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid arthritis.
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17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00651451.
15-SEP-2000; 2000US-00663870.
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Matches 145; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT
                                                                                                                                                                   or
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 852; DB 3; Length 145; 100.0%; Pred. No. 7e-77;
                                          Guegler KJ, Corley NC, Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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Gaps

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Asundi

Chen R,

(HYSE-) HYSEQ INC

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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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                                                                                                                                    Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, apolipoprotein, lipase, lipoprotein receptor, ALLr, angina, cardiovascular disease, lipid metabolism, myocardial infarction; cerebral ischaemia, arterial thrombosis; thrombolytic, antilipaemic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25. .145
/note= "Human mature CG95 (or C870) protein"
                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 852; DB 4; Length 14
100.0%; Pred. No. 7e-77;
"" "" " " Indels
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                                            Wang Z,
                                          Qian XB, Wang
J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .24
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNLDTYQKRLRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNLDTYQKRLRFYWRPHCRGQTPGC 145
                                                                                                                                                                                    Claim 20; Page 1102; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (or C870) lipase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE11924 standard; protein; 145 AA
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                                        Zhou P, c
A. Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                             protein of the invention
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                                                                                      WPI; 2001-476164/51.
N-PSDB; AAH98759.
                                                          Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                            Liu C,
                                                                                                                                                                                                                                                                                                                                                            Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200179446-A2
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                                          rang YT,
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                                                            Cao Y,
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The invention relates to polynucleotides encoding proteins CG122, CG179, CG95, CG121, CG162, CG179, CG185, CG170, CG183 and CG168 which are related to proteins involved in lipid metabolism and cardiovascular disease such as human apolipoproteins, lipsaes and lipoprotein receptor proteins. These DNA and protein sequences are useful for treating or preventing disorders associated with apolipoproteins, lipsaes and lipoprotein receptor (ALLr) expression and for treating ipid metabolism, cardiovascular diseases and thrombosis. Antibodies against these proteins are useful for determining the presence of or predisposition to a disease associated with altered levels of these sequences. ALLr polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them and cells expressing ALLr proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of this polypeptide. Vectors comprising these DNA and protein sequences are also useful for producing ALLr proteins.

The nucleic acids and polypeptides of the invention are also useful for the treatment of occlusive cardiovascular diseases.
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                                                                                                                                                                                   odrich R;
Qian XB;
                                                                                                                                                                                                                                                                                                                      and lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infarction, cerebral ischaemia, angina, arterial thrombosis, coronary artery thrombosis on intracardiac thrombosis and stroke. The nucleotides of the invention are used in getherapy. The present sequence is human CG95 (or C870) lipase protein
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                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human apolipoproteins, lipases, and lipoprotei receptor polypeptides, useful for preventing diagnosing and treating lipid metabolism disorders, thrombosis and cardiovascular diseases.
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YT, Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 852; DB 4; Length 145; 100.0%; Pred. No. 7e-77; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                     Tang TY, Zho
Drmanac RT,
                                                                                                                                                                                     D, Montgomery JR,
Zhao QA, Wehrman T,
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                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Fig 1; 266pp; English
                               2000US-0197137P.
2000US-00598042.
2000US-00631451.
2000US-00667298.
2000US-00114936.
16-APR-2001; 2001WO-US012529
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Best Local Similarity 100.0
Matches 145; Conservative
                                                                                                                                                                                     Loeb
V, Z
                                                                                                                                                                                                                                                                2001-611724/70
                                                                                                                                                  (HYSE-) HYSEQ INC.
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Asundi
                                                                                        22-SEP-2000;
                                   14-APR-2000;
                                                                     03-AUG-2000;
                                                                                                              17-NOV-2000;
                                                     20-JUN-2000;
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                                                                                                                                                                                     Ballinger
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                                                                                                                                                                                                                           Wang D;
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Length 145;

61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120

Human, cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antiannemic; anaemia; antiaggregant; haemostatic; ullnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; attimus; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder; Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection. treatment and diagnosis of e.g. cancer, Claim 20; Page 278; 1217pp; English. 23-DEC-1999; 99US-00471275. 21-JAN-2000; 2000US-00488725. 25-APR-2000; 2000US-00552317. rang YT, Liu C, Drmanac RT; 22-DEC-2000; 2000WO-US035017 neurological disorder. 2001-457603/49. (HYSE-) HYSEQ INC. N-PSDB; AAH99768 WO200153455-A2 Homo sapiens 26-JUL-2001

they are expressed in, such as: antinflaematory, antirheumatic, antiarthritic; immunosuppressive; antiantlaematory, antirheumatic; antiarthritic; immunosuppressive; antianterial; endocrine, cardiant; central nervous system; virucide; anti-HIV; fungicide; antianutagen; cardiovascular; antianemic; antiadgaregant; haemostatic; vulnerary; antianemic; antianterial; antiallergic; antiasthmatic; antiallergic; antiasthmatic; antianterial; neuroprotective; antialepressant; noctropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for sponding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, antenimunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, cancemia, platelet disorders, thrombocytopaenia, allergic chinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and neurological disorders AAH99166 to AAH99904 encode the human proteins given in AAW25225 to AAW25963. The proteins can have activities based on the tissues and cells

1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60 100.0%; Score 852; DB 4; Length 150; 100.0%; Pred. No. 7.3e-77; 0; Mismatches Query Match
Best Local Similarity 100.
Matches 145; Conservative Sequence 150 AA;

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Gaps

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0; Indels

nutional immunodeficiency virus; antiateriote; viruerary;

mutional immunodeficiency virus; antiasthmatic; vasotropic; cardiant;

muti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant;

muti-manic; immunosuppressive; cerebroprotective; antimicrobial;

antiinflammatory; antiabetraial antipsoriatic; thyromimetic;

immunomodulator; antiseborrheic; dermatological; vasoconstriction;

gastrointestinal disorder; cardiovascular disorder; hypertension;

coronary heart disease; arteriosclerosis; anorexia; obestry; bulimia;

cachexia; male infertility; impotence; testicular cancer; lung tumour;

hyperpoliferative disorder; bone disorder;

neurodegenerative disease; Alzheimer's disease; Parkinson's disease;

Muntington's disease; Alzheimer's disease; Parkinson's disease;

Muntington's disease; schizophrenia; mania; dementia; paranoia;

Muntington's disease; schizophrenia; mania; dementia; paranoia;

psychosis; autism; sleep disorder; immune system disorder;

Mashimoto's thyroiditis; musculo-skeletal system disorders; 125 multiple sclerosis; ischaemic brain injury; stroke; infectious disease; diabetes mellitus; immunological disorder; asthma; AIDS; immunogen; acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis; inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus; neural system disorder; respiratory disorder; olfactory disorder; Endress GA; Human, novel human protein, NHP, antidiabetic, antirheumatic, antiarthritic, cytostatic, antiarteriosclerotic, vulnerary, Gentz RL, 52. .65 /label= Immunogenic_epitope 67. .78 /label= Immunogenic_epitope /label= Immunogenic_epitope 121. .129 /label= Immunogenic_epitope 136. .141 /label≈ Immunogenic_epitope Coleman TA, 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145 Location/Qualifiers AAU09096 standard; protein; 145 Soppet DR, 03-APR-2000; 2000US-0194118P. 29-SEP-2000; 2000US-0236384P. (HUMA-) HUMAN GENOME SCI INC. 02-APR-2001; 2001WO-US010542 Novel human protein NHP #5. (first entry) .105 Moore PA, Ni J, Li Y, Dillon PJ; WO200174896-A1 wound healing Homo sapiens, 11-OCT-2001. 20-DEC-2001 AAU09096; 99 Region Region Region Region Region AAU09096 g g à

WPI; 2001-626394/72

us-09-830-321a-1.rag

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that encode them and antibodies raised against them. The proteins, antibodies are useful in the diagnosis, prognosis, prevention and/or treatment or diseases and/or disorders involving vasoconstriction, gastrointeerinal disorders, cardiovascular disorders (e.g. hypertension, erectile dysfunction, high blood pressure, coronary leart disease and arteriosclerosis), anorexia, obesity, bullimia, cachexia, disorders of small intestine, disorders of reproductive system, cachexia, disorders of small intestine, disorders of pulmonary system, can other hyperproliferative disorders, disorders of pulmonary system, central nervous system disorders, disorders, disorders, parkinson's diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, mania, dementia, paranoia, psychoses, autism, sleep disorders), immune system disorders, central nervous system disorders (e.g. multiple sclerosis, ischaemic brain injury and/or stroke), infectious diseases, diabetes mellitus, central nervous system disorders (e.g. multiple sclerosis, ischaemic brain injury and/or stroke), infectious diseases, diabetes mellitus, immunological disorders (e.g. asthma, acquired immunodeficient syndrome (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, psoriasis and lupus erythematosus), neural system (AIDS), aches, psoriasis and lupus erythematosus), neural system disorders, elsepiratory disorders, olfactory disorders and wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the nucleic acids
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                                         New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular disorders, autoimmune disorders and reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted group IID phospholipase A2 (sPLA2) enzyme.
                                                                                                                                                                                        relates to novel human proteins (NHP) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents an NHP of the invention
                                                                                                                                       Claim 11; Page 306-307; 318pp; English.
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N-PSDB; AAS14884
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                                                                                                                                                                                     The invention
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ABR44234
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The Invention Laters to a mammanian sector of 3 top in sector of phospholipase A2 (SPLA2) (1), where the entryme is Ca2+ dependent, phospholipase A2 (SPLA2) (1), where the entryme is Ca2+ dependent, composition comprising (1) is useful for treating or preventing viral and composition comprising (1) is useful for treating or preventing viral and composition compraining capable of inhibiting catalytic activity of (1), biologically active compounds that bind sPLA2 receptors, or a compound that modulates cell roliferation, cell migration, cell contraction or apoptosis is useful for treating disease states or disorders involving group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain ischaemia, acute lung injury, acute respiratory distress syndrome or crohn's disease. Specific antibodies are useful for searching new secreted mammals. The encoding polymucleotides and vectors are useful for transforming animals and establishing a line of transgenic animals.

**Coth of the compound of transforming animals are such the dIFF sPLA2 enzyme

**Coth of the coth of transforming animals are useful for transforming animals are such the dIFF sPLA2 carging to the animals.
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                                                                                                                                                                          Novel mammalian secreted group IIF secreted phospholipase A2, useful for preventing and treating bacterial and viral infections, and cancers.
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                                                                                                                                                                                                                                                                           invention relates to a mammalian secreted group IIF secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.3%; Score 846; DB 6; Length 14
99.3%; Pred. No. 2.8e-76;
iive 0; Mismatches 1; Indels
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                                                                                             Valentin E;
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                                                                                                                                                                                                                                    Disclosure, Fig 1; 33pp; English.
                                                       (CNRS ) CNRS CENT NAT RECH SCI.
                12-OCT-2001; 2001WO-IB002407.
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Best Local Similarity 99.33
Matches 144, Conservative
                                                                                                                                    WPI; 2003-403216/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 145 AA;
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                                                                                               Jazdunski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.3%;
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Best Local Similarity 99.3
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                           Lambeau G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases or ischemia,
                                                                                                                                                                                                                                                                   (LAMB/) LAMBEAU G. (VALE/) VALENTIN E.
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-567302/53.
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                                                                                                                            US2003073087-A1
                                                                                                                                                                                                                                                                                                                                         Lazdunski M,
                                                                                          Homo sapiens
                                                                                                                                                               17-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                  righties the sequence of an isolated inductor and mouration which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in regulated gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid, (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a cancer of the nucleic acid is useful for therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, carvix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in the control of the pathology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
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                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an isolated nucleic acid molecule, which
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                                                                                                                                                                                                                                                               New genes that are up-regulated or down-regulated in cancers, useful a markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic, antiinflammatory, vasotropic, cerebroprotective, sPLA2;
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                                                                                                                                                               Wilson KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 145;
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                                                                                                                                                             Hevezi PA, Mack DH,
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                                                                                                                          (EOSB-) EOS BIOTECHNOLOGY INC
            20-SEP-2001, 2001US-0323887P.
13-WOV-2001, 2001US-0350666P
08-FEB-2002, 2002US-035145P.
08-FEB-2002, 2002US-0352527P.
12-APR-2002, 2002US-0372246P.
                                                                                                                                                           Gish KC,
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                                                                                                                                                             Aziz N,
                                                                                                                                                                                                                               N-PSDB; ACC72857
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pathologies
                                                                                                                                                                             Zlotnik A;
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The invention describes a mammalian secreted group IIF phospholipase A2 (SPLA2), which is Ca2+-dependent, maximally active at pH of about 7-8, and hydrolyses phosphatidylelyen with about a 15-fold preference. The mammalian secreted group IIF SPLA2 protein or nucleic acid, or a pharmaceutical composition is useful for treating and/or preventing viral infections, bacterial infections, or cancers. The inhibitors of SPLA2 or a composition comprising sPLA2 inhibitors is useful for treating disease states or disorders involving group IIF SPLA2, e.g. inflammatory diseases, cancer, cardiac and brain ischaemia, acute lung injury, acute respiratory distress syndrome, or Crohn's disease. The enzyme is also useful for screening various chemical compounds for treating these diseases. This is the amino acid sequence of human group IID phospholipase A2 used to determine a consensus sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mammalian secreted group IIF phospholipase A2 or nucleic acid, use for treating or preventing viral or bacterial infections, or cancers, screening inhibitors of the enzyme for treating e.g. inflammatory
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viral infection; bacterial infection; cancer; inflammatory disease; cardiac ischaemia; brain ischaemia; acute lung injury; acute respiratory distress syndrome; Crohn's disease; enzyme.
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Pred. No. 2.8e-76;
); Mismatches 1;
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JP2000166544-A.
                                                    Mus musculus
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                                                                                                       Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                          Human secretory phospholipase A2 (PLA2) and its encoded gene for diagnosis and treatment of secretory PLA2-associated diseases e.g. septic shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
     Secretory phospholipase A2; PLA2; antiallergic; antiinflammatory; antibacterial; immunosuppressive; tranquillser; vulnerary; antirheumatic; antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis; chronic rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                             PLA2 has antiallergic, antiinflammatory, antibacterial, tranquillser, immunosuppressive, vulnerary, antitheumatic and antiarthritic activities. Human secretory phospholipase A2 (PLA2), the gene encoding it and antibodies against it are useful for the diagnosis and treatment of secretory PLA2-associated diseases e.g. septic shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The present sequence represents mouse PLA2, which is used in an example from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWCCQKHDCCYAHLKIDGCKSLTDNYKYSISQCTIQCSDNGSWCERQLCACDKEVALCLK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
                                                                                                                                                                                                                                                                                                                                                                                    present invention describes human secretory phospholipase A2 (PLA2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.3%; Score 624.5; DB 3; Length 71.0%; Pred. No. 3.2e-54; ive 14; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145
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|ONLDSYNKRLRYYWRPRCKGKTPAC 144
                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                        Hanasaki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNLDTYQKRLRFYWRPHCRGQTPGC
                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 37; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB11994 standard; protein; 144 AA
                                                                                           1. .19
/label= signal
                                                                                                                                                                                           99WO-JP006844.
                                                                                                                                                                                                                98JP-00349608.
                                                                                                                          /label= PLA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 71.0%;
tes 103; Conservative 1
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                                                                                                                                                                                                                                   (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                        Suzuki N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention
                                                                                                                                                                                                                                                                            WPI; 2000-423429/36
                                                                                                                                                                                                                                                                                       N-PSDB; AAA60866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 144 AA;
                                                                                                                                               WO200034486-A1
                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-NOV-2000
                                                                                                                                                                                                               09-DEC-1998;
                                                                                                                                                                                                                                                        Ishizaki J,
                                                                                                                                                                      15-JUN-2000
                                                                                                                                                                                                                                                                                                                                          arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                           Peptide
                                                                                                                 Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DWCCQKHDCCYAHLKIDGCKSLTDNYKYSISQGTIQCSDNGSWCERQLCACDKEVALCLK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a mouse secreted phospholipase A2 (secreted database, and a fragment (AAA7207) was isolated from CDNA derived from several mouse tissue types using primers AAA72078-A72081). The full length cDNA was generated using primers AAA72082-A72081. The full relates to the novel secreted PLA2, nucleic acids encoding it, and variants of the protein which retain phospholipase A2 activity. It also encompasses an expression vector and host cells comprising DNA encoding murine secreted PLA2, a method for the recombinant production of the protein, a method of screening potential inhibitors of the protein and the compounds thus identified, and an antibody specific for murine PLA2. The antibody can be used for the diagnosis of a variety of diseases
                                                           Secreted phospholipase A2; PLA2; mouse, murine; recombinant production; antibody; diagnosis; drug screening; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.3%; Score 624.5; DB 3; 71.0%; Pred. No. 3.2e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                      'note= "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse secretion type phospholipase A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 10-11; 12pp; Japanese.
                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB24434 standard; protein; 116
Mouse secreted phospholipase A2.
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es 103; Conserv
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61 DWCCQTHDCCYDHLKTQGCGIYKDN----NKSSIHCMD----LSQRYC 100

AAY99450 standard; protein; 116

RESULT 13

AAY99450

Human PRO1561 (UNQ768) amino acid sequence SEQ ID NO:378.

(first entry)

08-AUG-2000

AAY99450;

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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA7721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillan KJ;
Kuo SS, Paoni NF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.7%; Score 500.5; DB 3; Lengun ... 82.6%; Pred. No. 5.5e-42; ... wiematches 6; Indels
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Klein RD,
Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 72; Fig 94; 315pp; English.
                                                                                                                                                                                                                       99WO-US005028.
99US-0123957P.
99US-0131445P.
99US-0134287P.
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99US-0141037P.
99US-0144758P.
99US-0145698P.
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99US-0115554P.
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99WO-US021547
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                                                                                                                                                                                                                                                                                                                                                                                                                   -US023089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goddard A, Godowski PJ
Smith V, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    -SN66
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90; Conserv
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                                                                                      WO200032221-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi AJ,
                                                          Homo sapiens.
                                                                                                                                              30-NOV-1999;
                                                                                                                  08-JUN-2000
                                                                                                                                                                                                                                                      28-APR-1999
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Best Local S
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Human, PRO polypeptide, membrane bound protein, receptor, diagnosis, transmembrane, secretion, immunoadhesion, pharmaceutical, screening.
                                                                                                                                       98US-0098716P.
98US-0098749P.
98US-0098803P.
98US-0098803P.
98US-0098812P.
98US-0099536P.
98US-0099536P.
98US-0099542P.
98US-0099642P.
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98US-0101071P.
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                                                                               Homo sapiens.
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09-SEP-1998;
09-SEP-1998;
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09-SEP-1998;
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Conservative

Matches

DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLC 109

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9805-0101916P-
9805-0102207P-
9805-0102240P-
9805-0102307P-
9805-0102330P-
9805-0102331P-
9805-0102484P-
                                                           98US-0102487P.
98US-0102570P.
98US-0102684P.
98US-0102684P.
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9805-0103314P
9805-0103328P
9805-0103328P
9805-0103395P
9805-0103401P
9805-0103633P
9805-0103633P
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9805-0104257P

9805-0105000P

9805-0105164P

9805-0105169P

9805-0105693P

9805-0105693P

9805-0105693P

9805-0105881P

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9805-0105832P

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9805-010633P

9805-010633P
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98US-0108806P.
98US-0108807P.
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98US-0108848P.
98US-0108849P.
98US-0108850P.
98US-0108851P.
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07-0CT-1998

07-0CT-1998

07-0CT-1998

08-0CT-1998

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14-0CT-1998

14-0CT-1998

20-0CT-1998

20-0CT-1998
24-SEP-1998;
24-SEP-1998;
29-SEP-1998;
29-SEP-1998;
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29-SEP-1998;
29-SEP-1998;
30-SEP-1998;
30-SEP-1998;
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01-0CT-1998;
02-0CT-1998;
06-0CT-1998;
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22-0CT-1998;
22-0CT-1998;
26-0CT-1998;
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27-OCT-1998;
27-OCT-1998;
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27-0CT-1998;
28-0CT-1998;
28-0CT-1998;
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28-OCT-1998;
28-OCT-1998;
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29-OCT-1998;
29-OCT-1998;
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03-NOV-1998;
03-NOV-1998;
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03-NOV-1998;
10-NOV-1998;
17-NOV-1998;
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                                                                   30-SEP-1998
                                                                                                                  06-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                              30-OCT-1998;
03-NOV-1998;
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                                                                                                                                                                                     AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                       New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions.
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                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                      Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DWCCQTHDCCYDHLKTQGCGIYXDYYRYNFSQGNIHCSDKGSWCEQQLC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.7%; Score 500.5; DB 3; Length 116; 82.6%; Pred. No. 5.5e-42; ive 4; Mismatches 6; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eaton DL, Ferrara N,
                                      Watanabe CK,
                                      Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted; transmembrane; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers L,
                                                                                                                                                              Claim 12; Fig 222; 773pp; English
                                      Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB66199 standard; protein; 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein of the invention #111.
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99US-0144758P.
99US-0145698P.
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99WO-US030095.
2000WO-US000219.
2000WO-US000376.
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99US-0162506P.
99WO-US028313.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 82.6
nes 90; Conservative
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          (GETH ) GENENTECH INC
                                     Goddard A,
                                                                WPI; 2000-237871/20
                                                                               N-PSDB; AAA37132
                                                                                                                                                                                                                                                                                                                                  Sequence 116 AA;
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26-JUL-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
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16-DEC-1999;
05-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                      Baker K,
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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                                                                                                                                                                  The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; protetate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
              Watanabe CK;
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                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                useful as hybridization probes, in chromosome and gene mapping and gene
 Hillan KJ;
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                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                   transmembrane proteins and nucleic acids designated PRO,
                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                                                                                                                                                                                                                                                                                                                          DWCCQTHDCCYDHLKTQGCGIYKDN-----NKSSIHCMD----LSQRYC 100
                                                                                                                                                                                                                                                                                                           4; Length 116;
 L PJ, Grimaldi CJ, Gurney AL,
Smith V, Stewart TA, Tumas D,
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                           Score 500.5; DB 4
Pred. No. 5.5e-42;
                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO1561 polypeptide sequence.
                                                                                                                                         Claim 1; Fig 222; 787pp; English.
 Goddard A, Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU12438 standard; protein; 116
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99WO-US028551.
99WO-US028564.
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99US-0170262P.
99WO-US030095.
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2000WO-US000376.
2000WO-US003565.
                                                                                                                                                                                                                                                                                                           58.7%;
82.6%;
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             Paoni NF, Roy MA,
PM, Wood WI;
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                                                                                                                                                                                                                                                                                                                                       90; Conservative
                                                        WPI; 2001-071395/08.
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                Sequence 116 AA;
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Gao W, Goddan
Pan J, Paoni
Williams PM,
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06-JAN-2000;
11-FEB-2000;
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02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
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                                                                                    Secreted and
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20-DEC-1999;
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30-DEC-1999;
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ANUI2172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO breast, prostate, rectal, cervical or liver tumours by comparing PRO breast, prostate, rectal, cervical or liver tumours by comparing PRO olypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the peliferation of inner ear utricular supporting cells or of T-pyphocytes, the proliferation of endothelial cells or of T-pyphocytes, the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor villar. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymolectice encoding PRO involved in binding interactions. The polymolectice encoded in province to the province of the province to the province to the province of the province of the province to the province of the province of the province of the province to the province of the province to the province of the provin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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Pred, No. 5.5e-42;
4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Fig 534; 813pp; English.
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2000WO-US020710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-408281/43.
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Best Local Similarity
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                                                                                                                                                                                                                                                      03-MAR-2000;
10-MAR-2000;
15-MAR-2000;
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30-MAY-2000;
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02-MAR-2000;
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17-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/B_COMB.pep:*
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  5.1.6
Compugen Ltd.
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US-09-489-770-4
US-09-362-230-35
US-09-36-230-35
US-08-186-995-10
US-08-186-995-10
US-08-186-995-10
US-08-988-497-37
US-09-36-317-3
US-09-36-32
US-09-36-32
US-09-36-32
US-08-888-497-32
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US-08-170-360-5
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GenCore version (c) 1993 - 2004
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Pred. No. 1.1e-34;
                       US-08-688-497-30

US-09-1362-230-30

US-09-1362-230-30

US-08-888-497-44

US-09-1362-230-44

US-09-1362-230-44

US-08-130-44

US-08-130-44

US-08-130-43

US-08-130-22

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US-08-1362-230-22

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Sequence 4, Application US/08966317

Sequence 4, Application US/08966317

GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TILLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PRC
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: "FOLLOWS OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/966,317 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0403 US
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.1%;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: sin
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Best Local Similarity
LIBRARY: GenBa
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APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Marmalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
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61 TDWCCVTHDCCYNRLEKRGCGTKFLTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF 120
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ADDRESSEE: Russell PA
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Pred. No. 1.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Mismatches
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                                         120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
                                                                  STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
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                                                                                                                                                                   Sequence 35, Application US/08888497 Patent No. 5972677 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
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APPLICATION NUMBER: US 08
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.95
Matches 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305-764-4996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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MEDIUM TYPE: Floppy
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                                                                                                                     THDCCYDHIXTQGCGIYKDYYRYNFSQGNIHCSDKGSWGBQQHCACDKEVAFCL 119
                                                                                                                                                61 IDWCCVTHDCCYNRLERRGCGTKFLTYKFSYRGGISCSTNQDSCRKQLCQCDKAAAECF 120
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               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE AZ PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                  52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 401.5; DB 4
Pred. No. 1.1e-34,
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23; Mismatches
                  Mismatches
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APPLICATION NUMBER: US/09/489,770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPRENCE/DOCKET UNMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09489770 Patent No. 6399301
                                                                                                                                                                                                                                                                                                                                                                                  Hawkins, Phillip R.
Bandman, Olga
                 23;
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IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
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Best Local Similarity 47.2.
Local 70; Conservative
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                      Conservative
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MEDIUM TYPE: Diskett
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LIBRARY: General
Town 204319
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APPLICANT: Hawkin
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                      Matches
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US-08-186-895-10
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                                                      GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
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Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 70; Conservative 23; Mismatches 52; Indels 1.
                                                                                                                                                                                                                                    ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
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                                                                                                                                                                                                                                                                          200 East Broward Boulevard
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GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                      Sequence 35, Application US/09362230
Patent No. 6352849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 amino acids
                                                                                                                                                                                                                                                                                               Fort Lauderdale
                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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PCT-US94-07926-35
US-09-362-230-35
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Seilhamer, Jeffrey J.
WENTION: Mammalian Phospholipase A2 Nucleotide
Sequences and Low Moleotular Weight Amino Acid Sequences
VENTION: Sequences and Low Moleotide
VENTION: Encoded Thereby, Antisense Sequences and Nucleotide
VENTION: Sequences Having Internal Ribosome Binding Sites
EQUENCES: 44
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                        TITLE OF INVENTION: Manmalian Phospholipase A2 Nucleotide TITLE OF INVENTION: Sequences and Low Molecular Weight Am TITLE OF INVENTION: Encoded Thereby, Antisense Sequences TITLE OF INVENTION: Sequences Having Internal Ribosome Bi NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
47.0%; Score 400.5; DB 5
Best Local Similarity 47.9%; Pred. No. 1.4e-34;
Matches 70; Conservative 23; Mismatches 52
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Patent No. 5338885
GENERAL INFORMATION:
APPLICANT: Needham, Maurice R.C.
APPLICANT: Gooding, Clare
APPLICANT: Gooding, Clare
TITLE OF INVENTION: Expression Systems
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
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1615 L Street, N.W.
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APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UU-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: INTELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-JUL-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Manso, Peter J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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STREET: 16
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APPLICATION NUMBER: US/09/362,230
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                          32,264
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 46.4%
Best Local Similarity 47.6%
Matches 69; Conservative
                                                                                                                                                                                                                                                      NAME: Manso, Peter J. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                               305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                       APPLICATION NUMBER:
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-09-362-230-37
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                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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Patent No. 5972677

GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Become and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; Indels
                                                                                                                                                             OPERATING SYSTEM: PC-DOS/WS-DUS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,895
FILING DATE: 27-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION: A15
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/046,383
APPLICATION NUMBER: US/07/810,414
ATYORNEY/AGENT INPORMATION:
NAME: KOWILLS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TORRATION:
TELECOMMUNICATION TORRATION:
TELECOMMUNICATION TORRATION:
TELECOMMUNICATION TORRATION:
TELECOMMUNICATION TORRATION:
TELECOMMUNICATION TOR SOO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
munn: anino acids
munn: anino acids
munn: anino acids
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47.6%; Pred. No. 4.7e-34;
tive 23; Mismatches 52;
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                                                                                                                                                           PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                           COMPUTER READABLE FORM:
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Best Local Similarity
Matches 69; Conserva
                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
           Washington
                                   D.C.
: U.S.A.
                                                                       20036-5601
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US-08-888-497-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-186-895-10
                                                       COUNTRY:
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Sequence 37, Application US/09362230

Fatent No. 6352849
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences:
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nuclectide
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nuclectide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & CITY: Fort Lauderdale
CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DRCCVTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKODS-CRSOLCECDKAAATCFA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 144;
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.4%; Score 395.5; DB 2;
47.6%; Pred. No. 4.7e-34;
tive 23; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 RNKTTYNKKYQYYSNKHCRGSTPRC 144
                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/651,405
FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 305-527-2498
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                          US/08/888,497
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23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 RNKTTYNKKYQYYSNKHCRGSTPRC 144
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Patent No. 6103469
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
        TELECOMMUNICATION INFORMATION:
                     TELEPHONE: 305-527-2498
TELEPAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 aming acids
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
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Best Local Similarity 47.6%;
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INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                  69; Conservative
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                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                amino acid
                                                                                                                                                                         linear
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                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                  Matches
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APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell PA
STRBET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DWCCQTHDCCYDHLKTQGCGIYKDYRRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                46.4%; Score 395.5; DB 4; Length 144; 47.6%; Pred. No. 4.7e-34; Live 23; Mismatches 52; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNLDTYQKRLRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 1N21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-27-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Manso, Peter J. REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
                                                            US 08/097,354
          APPLICATION NUMBER: 08/888,497
FILING DATE: APPLICATION NUMBER: US 08/097,356
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application PC/TUS9407926 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       : 144 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nsa
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                                                                                                                                                                                                                                                                                                                                                                                     US-09-362-230-37
                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNPSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
                                                                                                                                                                                         61 DRCCVTRDCCYTRLEKRGCGTKFLSYKFSNSGSRITCAKQDS-CRSQLCECDCARAATCFA 119
                                                                                                            1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT
    Length 144;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Corley, Nail C.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
  DB 5;
Score 395.5; DB 5 Pred. No. 4.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,317
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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61 IDRCCVTHDCCXKSLEKSGCGTKLLKYKYSHQGGQITCSANQNSCQKRLCQCDKAAABCF 120
                                                                                               60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
                                               GSPKDA 60
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                                               CHCGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER KEALABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,360
FILING DATE: 03-MAR-1994
CLASSITCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU92/00333
FILING DATE: 06-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK 7058
FILING DATE: 04-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BETREE, BATDARA GA JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BATOR OF AUGUST OF AUGU
                                 1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYY
                                                                                                                                                                                                                                                                                                                                                                                             ; Section 18/08170360
; Patent No. 565662
; GENERAL INFORMATION:
; APPLICANT: TSENG, Albert P. S.
APPLICANT: TSENG, Adam
; TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
; CORRESPONDENCE: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell; Figg Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CTIY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.1%; Score 367.5; DB 1;
ilarity 51.6%; Pred. No. 3.4e-31;
Conservative 16; Mismatches 43;
                                                                                                                                                                                                                                                        120 KRNLDTYOKRLRFYWRPHCRGOTPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202)783-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss: single
linear
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Best Local Similarity
Matches 64; Conserv
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: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                   61 TDRCCCVTHDCCYKSLEKSGCGTKLLKYKYSHQGQQ1TCSANQNSCQKRLCQCDKAAAECF 120
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                            1 MELALLCGLVVMA-GVIPIQGGILNINKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA
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                                                                                                                      DB 3; Length 146;
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                                                                                                                43.6%; Score 371.5; DB 3; Length 47.3%; Pred. No. 1.6e-31; Live 19; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hawfins, Phillip R.
APPLICANT: Gandeler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
TILLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.6%; Score 371.5; DB 4;
47.3%; Pred. No. 1.6e-31;
tive 19; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Fast SEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/966,317
FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 KRNLDTYQKRLRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ARNKKTYSLKYQFYPNMFCKGKKPKC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0403 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09489770 Patent Nq. 6399301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 146 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 47.33
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3174 Porter Dr
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   650-845-4166
                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                               Best Local Similarity Matches 69; Conserv
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                                       984837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                   LIBRARY:
                         ; CLONE: 5
US-08-966-317-3
                                                                                                                         Query Match
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us-09-830-321a-1.rai

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REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFCATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/888,497
FILING DATE:
APPLICATION NUMBER: US 08/097,35-
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: MAISO, PETER J.
REGISTRATION NUMBER: 32,264
                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                               Sequence 39, Application US/09362230
Patent No. 6352849
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 amino acids
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Matches 64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: six
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                             US-09-362-230-39
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                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                  APPLICANT: Tischfield, Jay A.
APPLICANT: Sellhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences and Low Molecular Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
62 KFLSYKFSNSGSRITCAKQDS-CRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 YKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 KFLSYKESNSGSRITCAKQDS-CRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ILINLINKMVKQVTGKMPILSYMPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 124;
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.1%; Score 367.5; DB 2
51.6%; Pred. No. 3.4e-31;
tive 16; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 08/097,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/888,497
                                                                                                                                                                        Sequence 39, Application US/08888497
Patent No. 5972677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION UNDMER: 32,264
REFRENCE/DOCKET NUMBER: IN21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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Best Local Similarity
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STRANDEDNESS: sin
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                                                                                                                                                                                                                  GENERAL INFORMATION:
                                     142 TPGC 145
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                                                                            121 TPRC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                      US-08-888-497-39
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APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 KFLSYKFSNSGSRITCAKQDS-CRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGS 120
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                                                                                                                                                                                                                                                                                      ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.1%; Score 367.5; DB 4;
51.6%; Pred. No. 3.4e-31;
tive 16; Mismatches 43;
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APPLICANT: Weiss, Jerrold
APPLICANT: Elsbach, Peter
APPLICANT: Liang, Ning-Sheng
TILE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
TILE REFERENCE: 5986/1E917081
CURRENT APPLICATION NUMBER: US/09/740,569
CURRENT APPLICATION NUMBER: US 60/172,467
PRIOR PILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 124
TYPE: PRIOR PILING
TYPE: PATENTH: 124
TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
43.1%; Score 367.5; DB 4; Length 124;
Best Local Similarity 50.8%; Pred. No. 3.4e-31;
Matches 63; Conservative 18; Mismatches 42; Indels 1; Gaps
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Search completed: October 5, 2004, 19:24:54 Job time : 10.0867 secs

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TITLE OF INVENTION: NATERIALS AND METHODS RELATING TO LIPID METABOLISM FILE REPERRICE: 28110/35915A CURRENT APPLICATION NUMBER: US/09/835,996A CURRENT FILING DATE: 2001-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR PEDICATION NUMBER: US 60/197,137
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR PLILING DATE: 2000-09-22
PRIOR PELLING DATE: 2000-09-22
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PRICATION NUMBER: US 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR PRICATION NUMBER: US 09/598,042
PRIOR PRILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 6
SEQ ID NO 6
TYPE: PRI
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APPLICANT: Ballinger, Dennis APPLICANT: Loeb, Debra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Montgomery, Julie
Tang, Y. Tom
Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
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Asundi, Vinod
Zhao, Qing
Wehrman, Tom
Drmanac, Radoje
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qian, Xiahong
Wang, Dunrui
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Sequence 7, Appli
                                                                                                                                                       5, 2004, 19:25:05; Search time 32.8667 Seconds (without alignments) 1419.702 Million cell updates/sec
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Sequence 1342, A
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1 MELALLCGLVVMAGVIPIQG......YQKRLRFYWRPHCRGQTPGC 145
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6: \cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB.pep:*

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13: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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18: \cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-969-384-17

US-09-975-456B-7

US-09-946-374-378

US-10-147-493-534

US-10-147-493-534

US-10-16-503-534

US-10-16-503-534

US-10-144-993-534

US-10-158-787-534

US-10-16-6485-378

US-10-10-64-834-378

US-10-013-9078-378
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US-10-296-115-1342
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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5-499A-37	-910A-3	2-405-53	7-852A-5	7-900A-5	3-685A-5	5-254A-3	L-820A-	2-886-53	-728-53	-786-53	-499-53	-798-53	-395A-37	-072-53	-049-53	-904-53	-470-53	5-746-53	6-918-534	-921-53	Š	-474-53	-431 - 53	-114-5	-002-53	-856A-37	-419-53	-262-53	-423-53	
-10-	US-10-013	-10-	-10-	10-	-10-12	-10 - 22	-10-13	-10 - 14	-	-10	-10	US-10-157	-10	-10	-10	-10	2	-10-17	-10-17	-10-17	-10-13	10-14	-10-14	-10-1	10-14	•	-10-14	t	US-10-142	
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116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	
58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	58.7	
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ALIGNMENTS

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PRIOR FILING DATE: 2000-04-03
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Publication No. US20020192749A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT055P1

TUTLE OF INVERTION: HUMBER: US/09/969,384

CURRENT APPLICATION NUMBER: US/09/969,384

CURRENT FILING DATE: 2001-10-03

PRIOR FILING DATE: 2001-04-02

PRIOR FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: 60/236,384

PRIOR APPLICATION NUMBER: 60/194,118
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                                                                                                                                                   1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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APPLICANT: Hyerg inc.
TITLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
THE REPERENCE: T04PCT
CURRENT APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MBLALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT
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                                                         query Match
100.0%; Score 852; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.6e-81;
Matches 145; Conservative 0; Mismatches
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; Sequence 1342, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
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SEQ ID NO 1342
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ORGANISM: Homo sapiens
                 ORGANISM: Homo sapiens
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US-09-969-384-17
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US-09-835-996A-6
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APPLICANT: VALENTIN, EMMANUEL
TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
FILE REFERENCE: 14798 R-00
CURRENT APPLICATION NUMBER: US/09/975,456B
CURRENT FILING DATE: 2002-08-27
PRIOR RILING DATE: 2000-10-11
PRIOR FILING DATE: 2000-10-11
SEQ ID NOS: 10
SOFTWARE: PATENTIN VETSION 2.1
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99.3%; Pred. No. 6.7e-81;
tive 0; Mismatches 1; Indels
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Pred. No. 6.7e-81;
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US-09-946-374-378
Sequence 378, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 144; Conservative
                                                                                                                                                                                              Query Match
Best Local Similarity 99.3
Matches 144; Conservative
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                                                                         LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
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R APPLICATION NUMBER: 60/100684
R FILING DATE: 1998-09-17
R APPLICATION NUMBER: 60/100710
R FILING DATE: 1998-09-17
R APPLICATION NUMBER: 60/100711
R PILING DATE: 1998-09-17
                            FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100662
FILING DATE: 1998-09-16
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APPLICATION NUMBER: 60/101014
FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/101068
                                                                               APPLICATION NUMBER: 60/100664
FILING DATE: 1998-09-16
                                                                                                                                                                                                                                                                PPLICATION NUMBER: 60/100848
ILING DATE: 1998-09-18
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FILING DATE: 1938-09-18
APPLICATION NUMBER: 60/100919
FILING DATE: 1998-09-17
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APPLICATION NUMBER: 60/101279
                                                                                                                    APPLICATION NUMBER: 60/100683
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/100930
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APPLICATION NUMBER: 60/101071
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FILING DATE: 1998-09-23
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FILING DATE: 1998-09-23
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APPLICATION NUMBER: 60/101475
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FILING DATE: 1998-09-23
APPLICATION NUMBER: 60/101738
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APPLICATION NUMBER: 60/101477
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FILING DATE: 1998-09-24
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APPLICATION NUMBER: 60/101915
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FILING DATE: 1998-09-24
APPLICATION NUMBER: 60/102207
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FILING DATE: 1998-09-29
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FILING DATE: 1998-09-29
APPLICATION NUMBER: 60/102331
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FILING DATE: 1998-09-29
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FILING DATE: 1998-09-30
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APPLICATION NUMBER: 60/102684
                                                                                                                                       FILING DATE: 1998-09-17
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE PRESENCE: P2830PICI
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR PELICATION NUMBER: 60/098716
PRIOR PELICATION NUMBER: 60/098716
PRIOR PELICATION NUMBER: 60/098723
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   R APPLICATION NUMBER: 60/098723
R FILING DATE: 1998-09-01
NR APPLICATION NUMBER: 60/098749
R FILING DATE: 1998-09-01
R APPLICATION NUMBER: 60/098750
R FILING DATE: 1998-09-01
R PILING DATE: 1998-09-01
R R PLING DATE: 1998-09-02
R R PILING DATE: 1998-09-02
R R PILING DATE: 1998-09-02
R R PILING DATE: 1998-09-02
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FILING DATE: 1998-09-02
APPLICATION NUMBER: 60/099536
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APPLICATION NUMBER: 60/099816
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FILING DATE: 1998-09-09
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FILING DATE: 1998-09-09
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FILING DATE: 1998-09-09
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APPLICATION NUMBER: 60/099741
FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/099754
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099763
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APPLICATION NUMBER: 60/099792
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099808
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APPLICATION NUMBER: 60/099812
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APPLICATION NUMBER: 60/099815
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FILING DATE: 1998-09-15
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FILING DATE: 1998-09-16
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
                                                                                                                              Gurney, Austin L.
Hillan, Kenneth J.
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1998-09-23

1998-09-23

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1998-09-24

1998-09-30

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYBEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 93330R.C.252
CURRENT APPLICATION NUMBER: US/10/145,127
CURRENT FILING DATE: 2002-05-13
                                                                                                                                                                                                                    APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILLE REFERENCE: P3330R1C345
CURRENT APPLICATION NUMBER: US/10/147,493
CURRENT FILING DATE: 2002-05-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NOS: 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 116;
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Pred. No. 1.1e-44;
4; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 534, Application US/10145127 Publication No. US20040033558A1 GENERAL INFORMATION:
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Best Local Similarity 82.6%;
Matches 90; Conservative 4
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Stewart, Timothy A.
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Smith, Victoria
Stewart, Timothy A.
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Wood, William
Zhang, Zemin
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
Gerritsen, Mary E.
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Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
                      Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                   Tumas,Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapien
US-10-147-493-534
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 500.5; DB 10; Length 116;
Pred. No. 1.1e-44;
4; Mismatches 6; Indels 9;
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Publication No. US20040029217A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Filvaroff, Filen
APPLICANT: Gao, Wei-Qiang
  PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR PELING DATE: 1998-10-02
PRIOR PELING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-07
PRIOR PLING DATE: 1998-10-07
PRIOR PELING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/10316
PRIOR APPLICATION NUMBER: 60/10316
PRIOR PELING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR PELING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/10340
PRIOR PELING DATE: 1998-10-07
PRIOR PELING DATE: 1998-10-07
PRIOR PELING DATE: 1998-10-08
PRIOR PELING DATE: 1998-10-08
PRIOR PELING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103679
PRIOR PELING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103679
PRIOR APPLICATION NUMBER: 60/103711
PRIOR APPLICATION NUMBER: 60/103711
PRIOR APPLICATION NUMBER: 60/103711
PRIOR APPLICATION NUMBER: 60/10497
PRIOR PELING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/10500
PRIOR APPLICATION NUMBER: 60/10510
PRIOR APPLICATION NUMBER: 60/10510
PRIOR APPLICATION NUMBER: 60/10510
PRIOR APPLICATION NUMBER: 60/105693
PRIOR APPLICATION NUMBER: 60/105693
PRIOR PELING DATE: 1998-10-22
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l Similarity 82.6%;
90; Conservative
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Best Local S:
Matches 90
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Length 116;

DB 12;

58.7%; Score 500.5;

US-10-145-127-534

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Query Match

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1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACTUS ENCODING THE SAME
FILE REFERENCE: P3330R.1C28
CURRENT APPLICATION NUMBER: US/10/143,118
CURRENT APPLICATION NUMBER: US/10/143,118
PRIOR APPLICATION NUMBER: US/200-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330AC1261
CURRENT FILING DATE: US/10/144,993
CURRENT FILING DATE: 2002-05-13
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Pred. No. 1.1e-44;
4; Mismatches 6; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 500.5; DB 12; Length
Pred. No. 1.1e-44;
4; Mismatches 6; Indels
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Publication No. US20040038336A1
GENERAL INFORMATION:
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Best Local Similarity 82.6%;
Matches 90; Conservative 4
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                                                                                            Stewart, Timothy A.
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                               Gurney, Austin L.
                                                 Sherwood, Steven
Smith, Victoria
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Wood, William
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Gurney, Austin L.
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Filvaroff, Ellen
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Smith, Victoria
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US-10-143-118-534
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 90; Conserva
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TYPE: PRT
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LENGTH: 116
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                                                                                                          1 MELALLCGLVVMAGVIPIQGGILNINKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wacd, William
APPLICANT: Chang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C446
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 534
LENGTH: 116
                                             9; Gaps
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S8.7%; Score 500.5; DB 12; Length 116;

Best Local Similarity 82.6%; Pred. No. 1.1e-44;

Matches 90; Conservative 4; Mismatches 6; Indels 9;
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                                             Indels
82.6%; Pred. No. 1.1e-44; Mismatches 6;
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Publication No. US20040038335A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Perorge, Laura
APPLICANT: Perorge, Luc
APPLICANT: Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                      Sequence 534, Application US/10160503 Publication No. US20040033559A1 GENERAL INFORMATION:
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
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                                      90; Conservative
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Godowski, Paul
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; ORGANISM: Homo Sapien
US-10-160-503-534
               Best Local Similarity
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US-10-143-118-534
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Gaps

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Indels

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RESULT 13
US-10-140-808-534
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LENGTH: 116
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APPLICANT:
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APPLICANT: Tumas, Lanniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Mood, William
APPLICANT: Zanag, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C449
CURRENT APPLICATION NUMBER: US/10/158,787
CURRENT FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-17
PRIOR FILING DATE: 1997-09-17
PRIOR PRILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-09-19
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                                 1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
MELALLCGLVVMAGVIPIQGGILNIANKOVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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                                                                                                           DWCCQTHDCCYDHLKTQGCGIYKDN-----NKSSIHCMD----LSQRYC 100
                                                                                DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLC 109
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Pred. No. 1.1e-44;
4; Mismatches 6
                                                                                                                                                                                                                         ; Sequence 534, Application US/10158787; Publication No. US20040039164A1; GENERAL INFORMATION:
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Rivarcif, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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Best Local Similarity 82.6
Matches 90; Conservative
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ORGANISM: Homo Sapien
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US-10-158-787-534
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LENGTH: 116
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1 MELALLICGIVVMAGVIPIQGGILNINKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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FILE REFERENCE: P3330R1C69
CURRENT APPLICATION NUMBER: US/10/140,024
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
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Pred. No. 1.1e-44;
4; Mismatches 6; Indels 9;
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DWCCQTHDCCYDHLKTQGCGIYKDN-----NKSSIHCMD-
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                                                                                                                                   Sequence 534, Application US/10140024; Publication No. US20040058424A1; GENERAL INFORMATION:
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Watanabe, Colin K
Wood, William
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
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Gurney, Austin L.
Sherwood, Steven
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Best Local Similarity 82.6
Matches 90; Conservative
                                                                                                                                                                                                                                                                                   Desnoyers, Luc
Filvaroff, Ellen
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APPLICATION NUMBER: 60/099741
FILING DATE: 1998-09-10
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APPLICATION NUMBER: 60/099763
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APPLICATION NUMBER: 60/099812
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APPLICATION NUMBER: 60/099815
FILING DATE: 1998-09-10
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FILING DATE: 1998-09-10
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FILING DATE: 1998-09-10
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FILING DATE: 1998-09-15
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APPLICATION NUMBER: 60/100390
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APPLICATION NUMBER: 60/100584
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FILING DATE: 1998-09-16
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APPLICATION NUMBER: 60/100627
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FILING DATE: 1998-09-16
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FILING DATE: 1998-09-18
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APPLICATION NUMBER: 60/100684
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APPLICATION NUMBER: 60/100711
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FILING DATE: 1998-09-18
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FILING DATE: 1998-09-22
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FILING DATE: 1998-09-23
APPLICATION NUMBER: 60/101472
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APPLICATION NUMBER: 60/101738
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R.C182
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PTC9
CURRENT APPLICATION NUMBER: US/10/006,485A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/098716
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Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
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o. US20030064062A1
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R APPLICATION NUMBER: 60/098723
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R APPLICATION NUMBER: 60/098749
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APPLICATION NUMBER: 60/099596
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APPLICATION NUMBER: 60/099602
FILING DATE: 1998-09-09
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FILING DATE: 1998-09-02
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Hillan, Kenneth J
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Botstein, David
Desnoyers, Luc
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-534
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Best Local Similarity
Matches 90; Conserv
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GENERAL INFORMATION:
APPLICANT: Baker, K
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US-10-006-485A-378
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PRIOR PELICATION NUMBER: 60/101915

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PRIOR PELICATION NUMBER: 60/10207

PRIOR PELING DATE: 1998-09-29

PRIOR PELING DATE: 1998-09-30

PRIOR PELING DATE: 1998-09-30

PRIOR PELING DATE: 1998-09-30

PRIOR PELING DATE: 1998-09-30

PRIOR PELING DATE: 1998-10-07

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Pred. No. 1.1e-44;
4; Mismatches 6; Indels 9;
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                                                                                                                                                                                               Score 500.5; DB 1;
Pred. No. 1.1e-44;
4; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrara, Napoleone
Pong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
           PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/10581
PRIOR PLING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/10582
PRIOR APPLICATION NUMBER: 60/106023
PRIOR APPLICATION NUMBER: 60/106023
PRIOR FILING DATE: 1998-10-28
APPLICATION NUMBER: 60/105694
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Best Local Similarity 82.6%;
Matches 90; Conservative
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Hillan, Kenneth J
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Job time: 34.8667 secs
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US-10-013-907A-378
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Best Local Similarity
Matches 90; Conserv
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Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 5, 2004, 19:21:45; Search time 9.86 Seconds (without alignments) 1414.581 Million cell updates/sec

US-09-830-321A-1 852 1 MELALLCGLVVMAGVIPIQG......XQKRLRFYWRPHCRGQTPGC 145 Title: Perfect score: Sequence:

Scoring table:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	phospholipase A2 (phospholipase A2 (phospholipase A2 (phospholipase A2 (ď	K				phospholipase A2 (phospholipase A2 (phospholipase A2 (phospholipase A2 h		phospholipase A2 (phospholipase A2 (phospholipase A2 (phospholipase A2 (phospholipase A2 h	phospholipase A2 (se A	phospholipase a2 -
SUMMARIES	QΙ	A35493	A33394	PSHUYF	JU0283	148093	I48342	A49959	PSRSBT	151381	JX0052	PSRSB2	JC1342	813900	S68429	PSTVXF	S10992	E48188	PC4024	PSABA	JX0063	D48188	F48188	859522	PSSNAM	PSVIAC	S10333	I51386	SVIA	I50098
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o\c	Query Match]	47.1	46.9	46.4	45.7	45.7	42.9	40.7	39.4	39.4	39.0	•	œ.	37.6	37.5	7.		36.8	36.7	36.7	36.6	36.6	36.4	36.3	36.1		35.9	•	35.7	35.4
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123	158	138	138	122	122	124	137	130	138	120	122	138	138	122	122
35.0	34.7	34.6	34.4	34.1	33.9	33.9	33.8	33.7	33.7	33.5	33.5	33.4	33.3	33.2	33.1
298	295.5	295	293	290.5	288.5	288.5	288	287.5	287	285.5	285.5	284.5	283.5	283	282
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

us-09-830-321a-1.rpr

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A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 157, 488-493, 1988
A;Title: Phospholipase A-2 from human synovial flu
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A;Residues: 21-45, "X < PAR>
R;Recklies, A.D.; White, C.
Arthritis Rheum. 34, 1106-1115, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R, Lai, C.Y.; Wada, K.
                                                                                                                A; Accession: A32847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A31350
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Phospholipase A2 (EC 3.1.1.4) precursor (version 1) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Species: A33394, JU0131
R:Isbizaki, J.; Ohara, O.: Nakamura, E.; Tamaki, M.; Ono, T.; Kanda, A.; Yoshida, N.; Te
Biochem. Biophys. Res. Commun. 162, 1030-1036, 1989
A;Title: CDNA cloning and sequence determination of rat membrane-associated phospholipas
A;Reference number: A33394, MUD:89350908; PMID:2764915
A;Reference number: A33394, MUD:89350908; PMID:2764915
A;Reference number: A33394, MUD:89350908; PMID:2764915
A;Residues: 1-146 cish
A;Residues: 1-146 cish
A;Residues: 1-146 cish
A;Reference number: U00131; MUD:90110043; PMID:2606907
A;Title: Structure of CDNA coding for rat platelet phospholipase A2.
A;Residues: 1-146 ckCM>
A;Resi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phospholipase A2 (EC 3.1.1.4) IIA precursor [validated] - human

NiAlternate names: phosphatidylcholine 2-acylhydrolase; placental PLA2; platelet-secrete
C; Species: Homo saplens (man)
C; Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 15-Sep-2000
C; Accession: A22862; B32862; A60266; A32847; A60263; A31350; PT0056; A32913; A60265; A61
R; Kramer, R.M.; Hession, C.; Johansen, B.; Hayes, G.; McGray, P.; Chow, E.P.; Tizard, R.
J. Blol. Chem. 264, 5768-5775, 1989
A; Title: Structure and properties of a human non-pancreatic phospholipase A-2.
A; Reference number: A32862; MUID:89174633; PMID:2925633
A; Reference number: A32862; MUID:89174633; PMID:2925633
A; Residues: 1-144 < xRR.>
A; Molecule type: DNA
A; Residues: 1-144 < xRR.>
A; Molecule type: protein
A; Residues: 21-39 < xR2.>
A; Note: this protein was also detected in platelets
A; Note: this protein was also detected in platelets
A; Title: Structure and properties of a secretable phospholipase A-2 from human platelets
A; Reference number: A60266; MUID:91050834; PMID:2239446
A; Status: not compared with conceptual translation
A; Reference number: A60266; MUID:91050834; PMID:2239446
A; Status: not compared with conceptual translation
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Pred. No. 1.7e-29;
Transparence 52;
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A,Residues: 1-144 <KR3>
R;Seilhamer, J.J.; Pruzanski, W.; Vadas, P.; Plant, S.; Miller, J.A.; Kloss, J.; Johnson
J. Biol. Chem. 264, 5335-5338, 1989
A;Title: Cloning and recombinant expression of phospholipase A-2 present in rheumatoid a
A,Reference number: A32847; MUID:89174566; PMID:2925608
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ricrowl, R.; Stoner, C.; Stoller, T.; Pan, Y.C.; Conroy, R. Adv. Exp. Med. Biol. 279, 173-184, 1990
A; Title: Isolation and characterization of cDNA clones from human placenta coding for ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Phospholipase A-2 from human synovial fluid: purification and structural homolo
A;Reference number: A31350; MUID:89076274; PMID:3202859
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A;Reference number: PT0056; MUID:89197814; PMID:3240982
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A;Molecule type: protein
R;Residues: 21-46,/X',48-54 <HAR>
R;Residues: 21-46,/X',48-54 <HAR>
R;Kanda, A: Onc, T.; Yoshida, N.; Tojo, H.; Okamoto, M.
Biochem. Biophys. Res. Commun. 163, 42-48, 1989
Biochem. Biophys. Res. Commun. 163, 42-48, 1989
A;Title: The primary structure of a membrane-associated phospholipase A-2 from human spl
A;Reference number: A32913; MUID:89374261; PMID:2775276
A;Accession: A22913
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A,Residues: 21-144 (KAN)

R,Residues: 21-144 (KAN)

R,Parks, T.P.; Lukas, S.; Hoffman, A.F.

Adv. Exp. Med. Biol. 275, 55-81, 1990

Adv. Exp. Wiffliche: Purification and characterization of a phospholipase A-2 from human osteoarthri

A,Reference number: A60265; MUID:91050835; PMID:2146857
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A,Reference number: A61201; MUID:92029121; PMID:1930329
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A; Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 21-144
R; Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, B.R.; Gamboa, G.; Goods
Rater, C.; Warrick, M.W.; Jones, N.D.
Nature 352, 79-82, 1991
A; Title: Structure of recombinant human rheumatoid arthritic synovial fluid phospholipas
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R,Green, J.A.; Smith, G.M.; Buchta, R.; Lee, R.; Ho, K.Y.; Rajkovic, I.A.; Scott, K.F.
Riflammation 15, 355-366, 1991
A,Title: circulating phospholipase A-2 activity associated with sepsis and septic shock
A,Reference number: A61634; MUID:92098137; PMID:1757123
                                                                                                                                                                                                                                                                                                     A,Molecule type: mRNA
A,Residues: 1-144 <SEI>
A,Cross-references: GB:J04704; EMBL:M22430; NID:g190888; PIDN:AAA36550.1; PID:g190889
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A;Residues: 21-44 <GRE>
R;Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, Taater, C.; Marrick, M.W.; Jones, N.D.
submitted to the Brookhaven Protein Data Bank, May 1992
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A; Residues: 21-33 <LAI>
R; Hara, S.; Kudo, I.; Matsuta, K.; Miyamoto, T.; Inoue,
J. Blochem. 104, 326-328, 1988
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A, Contents: annotation; X-ray crystallography
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A,Gene: GDB:PLA2G2A, PLA2B, PLA2L A,Cross-references: GDB:120296; OMIM:172411

A; Map position: 1p36.1-1p35 A; Introns: 14/1; 62/2; 98/1

46.4%; Score 395.5; DB 1 47.6%; Pred. No. 3.9e-29; tive 23; Mismatches 52

69; Conservative

Similarity

Local Matches

В ð g ð

Query Match

121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

C; Accession: JU0283

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Rikennedy, B.P.; Payette, P.; Mudgett, J.; Vadas, P.; Pruzanski, W.; Kwan, M.; Tang, C.; J. Biol. Chem. 270, 2278-22385, 1995
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J. Shitlels. A natural disruption of the secretory group II phospholipase A2 gene in inbred n A; Reference number: I49352; MUID:95403435; PMID:7673223
A; Accession: I49352
C;Accession: I48093
R;Vial, D.; Senorale-Pose, M.; Havet, N.; Molio, L.; Vargaftig, B.B.; Touqui, L.
J. Biol. Chem. 270, 17327-17332, 1995
A;Title: Expression of the type-II phospholipase A2 in alveolar macrophages. Down-regulat
A;Reference number: I48093; WUID:95340522; PMID:7615534
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: I48342; PC2009; S35948; I49352
R;Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 195, 1254-1263, 1993
A;Title: Enhancing factor, a Paneth cell specific protein from mouse small iA;Reference number: I48342; MUID:94029955; PMID:8267767
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A;Cross-references: BMBL:X74266; NID:g557247; PIDN:CAA52325.1; PID:g557248
R;Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 197, 351-352, 1933
A;Title: Enhanching factor, a peneth cell specific protein from mouse small A;Reference number: PC2009; MUID:94071967; PMID:8250944
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A;Residues: 22-146 <MUL2>
A;Note: correction 0.855948
R;Mulherkar, R.; Rao, R.; Wagle, A.; Patki, V.; Deo,
submitted to the EMBL Data Library, July 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.7%; Score 389; DB 2;
49.3%; Pred. No. 1.5e-28;
tive 20; Mismatches 52
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A;Molecule type: mRNA
A;Residues: 1-145 <RES>
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A;Molecule type: mRNA
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C.Keywords: carboxylic ester hydrolase
F.68,113/Active site: His, Asp #status predicted
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Best Local Similarity 49.3*
Matches 72; Conservative
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A; Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-A; Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-A; Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice C; Superfamily: phospholipase A2
C; Keywords: calcium, carboxylic ester hydrolase; extracellular protein; lipid degradatic F; 12-20/Domain: signal sequence #status predicted <SIG>F; 21-144/Froduct: phospholipase A2 IIA #status experimental <MAT>F; 46-137, 48-64, 63-117, 69-144, 70-110, 79-103, 97-108|Disulfide bonds: #status experimental F; 47, 49, 51, 68/Binding site: calcium (His, Gly, Gly, Asp) #status predicted
F; 67, 111/Active site: His, Asp #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 IDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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C;Species: Cavia porcellus (guinea pig)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phospholipase A2 (EC 3.1.1.4) precursor (version 2) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep_1990 #sequence_revision 07-Sep-1990 #text_change 24-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TDWCCVTHGCCYNLLEKRGCGTKFLTYKFSYRGGQISCSTNQDSCRKQLCQCDKAAAECF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K. J. Biochem. 106, 545-547, 1989
J. Biochem. 206, SAS-547, 1989
A;Title: Structure of cDNA coding for rat platelet phospholipase. A;Reference number: JU0131; MUID:90110043; PMID:2606907
A;Accession: JU0283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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A, Residues: 1-146 < KON>
C, Superfamily: phospholipase A2
C, Keywords: carboxylic ester hydrolase
F,1-21/Domain: signal sequence #status predicted < SIG>
F,22-146/Product: phospholipase A2 #status predicted < MAT>
F,68,113/Active site: His, Asp #status predicted
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DB 2;

45.7%; Score 389.5; DB 2; llarity 47.3%; Pred. No. 1.4e-28; Conservative 23; Mismatches 53;

Similarity

Query Match Best Local S Matches 69

69;

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RESULT 5

I48093

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A,Molecule type: protein
A,Residues: 17-36 <LAN>
R,Faure, G.; Choumet, V.; Bouchier, C.; Camoin, L.; Guillaume, J.L.; Monegier, B.; Vuilh
Bur. J. Blochem. 223, 161-164, 1994
A,Title: The origin of the diversity of crotoxin isoforms in the venom of Crotalus duris
A,Reference number: 845646; MUID:94307256; PMID:8033889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-A, Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice (; Superfamily: phospholipase A2 (; Superfamily: phospholipase A2 (; Superfamily: phospholipase A2 (; Superfamily: phospholipase A2 (; St.) A (; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phospholipase A2 (EC 3.1.1.4) Mojave toxin basic subunit precursor - Mojave rattlesnake NyAlternate names: Mtx-B; phosphatidylcholine 2-acylhydrolase (;Species: Crotalus scutulatus scutulatus (Mojave rattlesnake) (;Date: 13-Sep-1996 #sequence_revision 14-Feb-1997 #text_change 11-Jun-1999 (;Accession: 151381, A35951 R;John, T.R.; Smith, L.A.; Kaiser, I.I. (Gene 139, 229-234, 1994 A;Title: Genomic sequences encoding the acidic and basic subunits of Mojave toxin: unusu A;Reference number: IS1380; MUID:94156205; PMID:8112610
                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 17-48, 'Q',50-76, 'Y',77-80, 'R',82-85,'K',87-114,'B',116-120,'B',122-138 <FRR
R; Landucci, E.C.T.; Condino-Neto, A.; Perez, A.C.; Hyslop, S.; Corrado, A.P.; Novello,
Coxicon 32, 217-226, 1994
A; Title: Crocxin induces aggregation of human washed platelets.
A; Reference number: A49841; MUID:94205018; PMID:8153961
                                                                                                                                                               Oxford, 1980 crotoxin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC
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    A; Residues: 17-80, R., 22-138 <AIR>
A; Note: 49-Gln, 53-Arg, and 85-Arg were also found
R; Fraenkel-Conrat, H.; Jeng, T.W.; Hsiang, M.
in Natural Toxins, Baker, D., and Wadstrom, T., eds., Pergamon Press, A,Title: Biological activities of crotoxin and amino acid sequence of A; Reference number: A94424
A; Accession: A94424
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46.3%; Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Comment: Crotoxin is a beta-neurotoxin. C; Complex: heterodimer of acidic and basic subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 17-138 <FA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL:X12603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phospholipase A2 (EC 3.1.1.4) low molecular weight, precursor - human c; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 10-Reb-1995 #sequence_revision 10-Reb-1995 #text_change 18-Jun-1999
C; Accession: A49959
R; Chen, J.; Engle, S.J.; Seilhamer, J.J.; Tischfield, J.A.
J. Biol. Chem. 269, 2365-2368, 1994
A; Title: Cloning and recombinant expression of a novel human low molecular weight Ca(2+)
A; Reference number: A49959; MUID:94131989; PMID:8300559
A; Reference number: A49959; MUID:94131989; PMID:8300559
A; Residues: 1-138 < CHE>
A; Residues: 1-138 < CHE>
C; Superfaminary
A; Roberne ces: GB:103090; NID:9460914; PIDN:AAC28886.1; PID:9460915
C; Superfamily: phospholipase A2
C; Superfamily: phospholipase A2
C; Keywords: carboxylic ester hydrolase
F; 67, 111/Active site: His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phospholipase A2 (EC 3.1.1.4) crotoxin basic subunit 1 precursor - tropical rattlesnake phospholipase A2 (EC 3.1.1.4) crotoxin basic subunit 1 precursor - tropical rattlesnake. S. Species Cotalus durissus terrificus (tropical rattlesnake, cascabel) C. Species 30-Unu-1988 #sequence revision 30-Sep-1991 #text change 11-Unu-1999 C. Accession: S02257, A90078; A9424; A49841; S45546; S46599; A26079; A28045; S46596 P. Rouchier, C.; Ducancel, F.; Guignery-Frelat, G.; Bon, C.; Boulain, J.C.; Menez, A. Nucleic Acids Res. 16, 9050, 1988 encoding the two subunits of crotoxin. A. Reference number: S01392; MUD:89016587; PMID:3174444 A. Molecule type: mRNA A. Molecule type: MUD:86293; MUD:86321988; PMID:3753003
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                                                                                                                                                                                                                                                                                                                               TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
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                                                                                                                                                                                                                                                                                                                                                                             TDRCCVTHDCCYKSLEKSGCGTKLLTYKYSHQGQLTCSANQNSCQKRLCQCDKAAAECF
                                                                                                                                                                                                                  1 MELALLCGLVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA
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                                                                                        Gaps
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H
        Length 146;
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                                                                                    Indels
42.9%; Score 365.5; DB 2;
47.3%; Pred. No. 2.2e-26;
live 18; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRNLDTYOKRLRFYWRPHCRGOTPGC 145
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RNLRSYNPQYQYF 132
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                                                                               Conservative
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Best Local Similarity
Matches 58; Conserv
                                 Local Similarity
les 69; Conserv
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        Query Match
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J. Biol. Chem. 267, 8846-8851, 1992
A;Title: Interleukin-1beta- and forskolin-induced synthesis and secretion of group II phc
A;Reference number: A38247; MUID:92250468; PMID:1577722
                                                                                                                                                                                                                                                                                                                                 A,Title: Purification and characterization of a membrane-associated phospholipase A2 from A,Reference number: A28618; MUID:88186890; PMID:3356705
A,Accession: A28618
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A; Residues: 1-138 <BOU>
A; Cross-references: BMBL:X16100; NID:962696; PIDN:CAA34227.1; PID:962697
A; Cross-references: BMBL:X16100; NID:962696; PIDN:CAA34227.1; PID:962697
A; Parks, T.P.; Lukas, S.; Hoffman, A.F.
Adv. Exp. Med. Biol. 275, 55-81, 1990
A; Title: Purification and characterization of a phospholipase A-2 from human osteoarthrit A; Reference number: A60265; MUID:91050835; PMID:2146857
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A;Residues: 17-41,'X' <PAR.
R;Festidues: 17-41,'X' <PAR.
R;Faure, G.; Choumet, V.; Bouchier, C.; Camoin, L.; Guillaume, J.L.; Monegier, B.; Vuilhc
Eur. J. Biochem. 223, 161-164, 1994
A;Title: The origin of the diversity of crotoxin isoforms in the venom of Crotalus duriss
A;Reference number: 845646; MUID: 94307256; PMID: 8033889
                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 'X',2-26,'X',28-36 <ONO>
A,Reperimental Source: spleen
R,Aarsman, A.J.; de Jong, Jong, Jong, Jong, Jong, Jong, F.W.; van Wassenaar, P.D.; Van
J. Biol. Chem. 264, 10008-10014, 1989
A,Title: Immunoaffinity purification, partial sequence, and subcellular localization of
A,Reference number: A33506; MUID:89255484; PMID:2722857
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                Pfeilschifter, J.; Maerki, F.; van den Bosch,
7, 8846-8851, 1992
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A;Residues: 1-25,'X',27,'X',29-33,'X',35-36,'X',38-40 <SCH>
R;Ono, T.; Tojo, H.; Kuramitsu, S.; Kagamiyama, H.; Okamoto,
J. Biol. Chem. 263, 5732-5738, 1988
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; Pred. No. 2.2e-23;
17; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47,92/Active site: His, Asp #status predicted
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C;Keywords: carboxylic ester hydrolase
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A, Molecule type: protein
A, Residues: 'D', 2-24 <AAR>
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Best Local Similarity
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A; Status: preliminary
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Ajmolecule type: protein
Ajacossion: Aj35921
Ajmolecule type: protein
Ajacossion: Aj26921
Ajmolecule type: protein
Ajacossion: 14/1; 58/2; 92/1
CjGenetics:
Ajntrons: 14/1; 58/2; 92/1
CjComplex: heterodimer of acidic and basic subunits
CjComplex: heterodimer of acidic and basic subunits
Ajntrons: 14/1; 58/2; 92/1
CjComplex: heterodimer of acidic and basic subunits
CjComplex: heterodimer of acidic and basic subunits
CjComplex: heterodimer of acidic and serionally enhanced when the phospholipid is condensed into a mice CjComplex: phospholipase A2
CjComplex: heterodimer; lipid degradation; metallocy; superfamily: phospholipase A2
CjComplex: heterodimer; lipid degradation; metallocy; phospholipase A2 basic chain #status experimental <Ax.
CjComplex: heterodimer; lipid degradation; metallocy; phospholipase A2 basic chain #status experimental <Ax.
F;11-18/Domain: signal sequence #status predicted F;20,80/Binding site: micellar substrate (GIn, Tyr) #status predicted F;2-131,44-60,59-111,65-138,66-104,73-97,91-102/Disulfide bonds: #status predicted F;63,105/Active site: His, Asp #status predicted
                                                     A;Residues: 1-138 <UOH>
A;Cross-references: EMBL:U01027; NID:g451317; PIDN:AAC59674.1; PID:g451318
A;Cross-references: EMBL:U01027; NID:g451317; PIDN:AAC59674.1; PID:g451318
B;Aird, S.D.; Kruggel, W.G.; Kaiser, I.I.
Toxicon 28, 669-673, 1990
A;Title: Amino acid sequence of the basic subunit of Mojave toxin from the venom of the A;Reference number: A35951; MUID:90385490; PMID:2402763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 24-Jul-1997
C;Accession: JX0052; A414318; A26924; A38247; A28618; A33506
F;Hayakawa, M.; Kudo, I.; Tomita, M.; Nojima, S.; Inoue, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYMPYGCHCGLGGRGQPKDATDWCCQTHDC
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A;Status: translated from GB/EMBL/DDBJ
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A;Residues: 'X',2-19 <HA2>
R;Hayakawa, M.; Horigome, F
J. Biochem. 101, 1311-1314,
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Matches 63; Conserv
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                                 Molecule type:
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phospholipase A2 (EC 3.1.1.4) - Bothrops asper
C;Species: Bothrops asper
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S13900
R;Francis, B.; Gutierrez, J.M.; Lomonte, B.; Kaiser, I.I.
Arch. Biochem. Biophys. 284, 352-359, 1991
A;Title: Myotoxin II from Bothrops asper (Terciopelo) venom is a lysine-49 phospholipase
A;Reference number: S13900; MUID:91112832; PMID:1899180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myotoxin precursor - southern copperhead
C;Species: Agkistrodon contortrix contortrix (southern copperhead)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: S68429; S7426
R;de Araujo, H:S.S.; White, S.P.; Ownby, C.L.
Arch. Biochem. Biophys: 326, 21-30, 1996
A;Title: cDNA cloning and sequence analysis of a lysine-49 phospholipase A(2) myotoxin fA;Reference number: S68429; MUID:96154243; PMID:8579368
A;Accession: S68429.
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A;Cross-references: EMBL:U21335; NID:g809484; PIDN:AAC59887.1; PID:g809485
A;Accession: S74296
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3.3e-22;
48;
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A;Residues: 17-36 <DER>
C;Superfamily: phospholipase A2
Ef:1-16/Domain: signal sequence #status predicted <SIG>
F;17-137/Product: myotoxin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.6%; Score 320.5; DB 2; ilarity 50.4%; Pred. No. 2.4e-22; Conservative 15; Mismatches 39;
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45.4%; Pred. No. 3.3e
cive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 1-12 <RRA
Superfamily: phospholipase A2
C,Seprerfamily: carboxylic ester hydrolase
123 YMTYPNILCSSKSEKC 138
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123 YKAYFKFKCK 132
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Matches 58; Conserv
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A; Status: preliminary
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                       A; Accession: 3-55-64, A; Accession: 3-55-64, A; Accession: 3-55-64, A; Accession: acid sequence not shown A; Status: nucleic acid sequence not shown A; Relatues: nucleic acid sequence acid sequence
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C;Species: Agkistrodon halys (halys viper)
C;Species: Agkistrodon halys (halys viper)
C;Accession: JC1342
R;Pan, H; Ou-Yang, L.L.; Yang, G.Z.; Zhou, Y.C.; Wu, X.F.
Acta Biochim, Biophys. Sin. 28, 579-582, 1996
A;Title: Cloning of the BPLA2 gene from Agkistrodon halys Pallas.
A;Reference number: JC1342
A;Reference number: JC1342
A;Reference number: JC1342
A;Residues: I-138 PAN
A;Residues: 1-138 PAN
A;Residues: L-138 Peph)
A;Note: the authors translated the codon GAC for residue 54 as Asn
C;Comment: This protein catalyzes specifically the hydrolysis of the C-2 ester bond of 3
C;Superfamily: phospholipase A2
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase
F;1-138/Product: phospholipase A2 #status predicted <NAT>
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43.4%; Pred. No. 5e-23;
tive 24; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.9%; Score 331.5; DB 1 44.1%; Pred. No. 2.7e-23; iive 21; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 LRFYWRPHCRGQTPGC 145
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phospholipase A2 (EC 3.1.1.4) X - habu
NyAlternate names: phosphatidylcholine 2-acylhydrolase
(Specials: Trimeresurus flavoviridis (habu)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 24-Apr-1998
C;Accession: A25500
R;Kini, R.W.; Kawabata, S.I.; Iwanaga, S.
Toxicon 24, 1117-1129, 1986
A;Title: Comparison of amino terminal region of three isoenzymes of phospholipases A2 (T quence of the basic phospholipase, TFV PL-X.
A;Reference number: A94320; MUID:87179112; PMID:3564060
A;Accession: A25500
A;Molecule type: protein
A;Reference number: A94320; MUID:87179112; PMID:3564060
A;Molecule type: protein
A;Reference number: actalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a mice C;Superfamily: phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; homodimer; lipid degradation; metallopr C;Superfamily: phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; homodimer; lipid degradation; metallopr F;26-122,28-44,43-95,49-115,50-88,57-81,75-86/Disulfide bonds: #status predicted F;47,89/Active site: His, Asp #status predicted

Ouery Match
37.1%; Score 316.5; DB 1; Length 122;
Best Local Similarity 46.8%; Pred. No. 5.6e-22;
Matches 58; Conservative 16; Mismatches 47; Indels 3.

5 22 ILNLNKAVVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGI 81 Gaps 3;

> qq à qq à g

142 TPGC 145

Search completed: October 5, 2004, 19:36:26 Job time : 10.86 secs

119 TEĞC 122

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us-09-830-321a-1.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 5, 2004, 19:13:29 ; Search time 5.8 Seconds (without alignments) 1301.754 Million cell updates/sec Run on:

US-09-830-321A-1

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 Total number of hits satisfying chosen parameters:

141681 seqs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Qgunk4 homo sapien Qgwvf6 mus musculu p14423 rattus norv p1455 homo sapien P47711 cavia porce p31482 mus musculu Qgbzm2 homo sapien P39877 homo sapien Qgyc4 mus musculu p07517 crotalus du Q02517 crotalus du Q03717 crimeresuru Q91391 mus musculu Q91319 pothrops as Q42187 agkistrodon Q94187 agkistrodon Q91319 bothrops pi P59264 trimeresuru Q00229 cchis color P6666 trimeresuru P58133 rattus norv P58139 bothrops pi P59264 trimeresuru P591433 rattus norv P58139 bothrops pi P59264 trimeresuru P591433 rattus norv P66860 trimeresuru P591433 bothrops pi P17935 vipera ammo Q90249 bothrops ja P04417 agkistrodon
SUMMARIES	PAZD HUMAN PAZD MOUSE PAZA HUMAN PAZA HUMAN PAZA HUMAN PAZA BOTAS PAZE HUMAN PAZE HUMAN PAZE HUMAN PAZE HUMAN PAZE GROUD PAZE GROUD PAZE GROUD PAZE MOUSE PAZE TRIFL
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% Query Match	0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.
Score	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Result No.	

P14421 agkistrodon Ogpvf3 agkistrodon P20381 trimeresuru Q92147 trimeresuru Q90w39 trimeresuru Q42188 agkistrodon	Q9nzk7 homo sapien Q9jiy9 trimeresuru P59071 daboia russ P04361 agkistrodon Q8uvu7 cerrophidio Q8uvz7 crotalus at
PA23 AGKHP PA2F AGKRH PA2J TRIFL PA2D TRIFL PA2P TRIMU PA29 AGKHP	PA2E_HUMAN PA2_TRIJE PA2B_DABRR PA2H_AGKPI PA2H_CERGO PA2H_CROAT
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311.5 311.5 311.5 310 309.5	308.5 308 307.5 307.5 307.5
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ALIGNMENTS

RESULT PA2D H ID P.	RESULT 1 PA2D HUMAN ID PA2D HUMAN STANDARD; PRT; 145 AA.
DEF	Q9UNK4, Q9URO1; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update)
DE	10-0CT-2003 (Rel. 42, Last annotation update) Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
	(Phospharidylcholine 2-acylhydrolase GIID) (GIID sPLA2) (PLA2IID) (SPLA(1)-IID) (Secretory-Lype PLA, stroma-associated homolog).
Sos	
ပ္ပပ္	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
× Z	NCBI_TaxID=9606; [1]
RP X	SEQUENCE FROM N.A., VARIANT GLY-80, AND CHARACTERIZATION.
A 6	Painter J. Suzuki W. Higashino KI., Yokota Y., Ono T.,
R.	"Cloning and characterization of novel mouse and human secretory
R.T.	phospholipase Azs."; J. Biol. Chem. 274:24973-24979(1999)
Z.	[2]
КЪ	SEQUENCE FROM N.A.
X &	MEDLINE=21040292; PubMed=11196711; Shakhow a M Pubrecky a V Tyothow 7 C Thomason a 17
2	Nedospasov S.A.;
RT	"SPLASH (PLA(2)IID), a novel member of phospholipase A2 family, is
R I	associated with lymphotoxin-deficiency.";
3 2	Genes inmun. 1:191-199 (2000). [3]
КP	SEQUENCE FROM N.A.
& ₽	Wallis J.; Submitted (OCT-2000) to the RMRL/GenBank/DDB.1 detabases
Z.	
7. P	SEQUENCE FROM N.A.
y x	TISSUE=Pancreas, and Spleen; MEDLINE=22188257: PuhMed=12477912.
\$	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
\$ 5	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg R., Ruetow K.H., Schaefer G.E., Phat N.Y.
\$:	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
5	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant דון, Scheeta די
\$	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
\$ 5	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
5 S	Bosak S.A., McEwan F.U., McKernan K.U., Malek J.A., Gunaratne P.H., Richards S. Worlev K.C. Hala S. Carris A.M. Carrist H. H.L., S.M.
≴:	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
5 5	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
5	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.
\$ 5	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
9.5	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: Broadly expressed. MISCELLANGOUS: Maximally active at neutral to alkaline pH and with
                                 human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. L-alpha-1-palmitcyl-2-linoleoyl phosphatidylethanolamine is more efficiently hydrolyzed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. GROUP IID SECRETORY PHOSPHOLIPASE A2.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001211; Phospholipia metabolism; TAS.
InterPro; IPR001211; PhospholipaseA2.
Print, Pr00068; PhospholipaseA2.
PRINTS; PR00303; PHPHILIPASEA2.
ProDom; P000303; PhospholipaseA2; 1.
SWART; SW0008; PA2c; 1.
PR05ITE; P800119; PA2 ASP; 1.
PR05ITE; P800118; PA2 HIS; 1.
Hydrolase; Lipid degradation; Signal; Calcium; Polymorphism.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
CALCIUM (VIA CARBONYL OXYGEN)
CALCIUM (VIA CARBONYL OXYGEN)
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CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO:0004624; F:secreted phospholipase A2 activity; TAS. GO:0006954; P:inflammatory response; TAS. GO:0006644; P:phospholipid metabolism; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 846; DB 1; Length 14
Pred. No. 1.7e-78;
0; Mismatches 1; Indels
                                                                                                                                                                 than the other phospholipids examined.

CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylglycerophosphochline + a fatty acid anion.

COFACTOR: Binds 1 calcium ion per subunit.
SUBCELLULAR LOCATION: Secreted (Potential).
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CF3A49DE516BD1EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the phospholipase A2 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005576; C:extracellular; TAS
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EMBL, AF188625, AAF09020.1; -.
EMBL, ALIS8172; CAC13159.1; -.
EMBL, BC025706, AAH25706.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16546 MW;
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HSSP; P14555; 1POD.
Genew; HGNC:9033; PLA2G2D.
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ACT SITE
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           SOLUTION OF THE STREET STREET
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rakawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S., Alazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H., Sasi C., King B., Yochiwa H., Rell P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Brownstein M., Bulk C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P., Ashordone P., Ringwald M., Rodriguez I., Sakamoto N., Satok M., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Alayashizaki Y.;
DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
                      Nedospasov S.A.; "SPLASH (PLA(2)IID), a novel member of phospholipase A2 family, is associated with lymphotoxin-deficiency."; Genes Immun. 1:191-199(2000).
                                                                                                                                                                                                                                             Q9WVF6; Q9JLK0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
(sphaghatidylcholine 2-acythydrolase GIID) (GIID spLA2) (PLA2IID)
FLA2G2D OR PLA2A2 OR SPLASH.
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99386983; PubMed=10455175; *
Ishizaki U., Suzuki N., Higashino K.-I., Yokota Y., Ono T.,
Kawamoto K., Fujii N., Arita H., Hanasaki K.;
"Cloning and characterization of novel mouse and human secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99115857; PubMed=10183420;
Walentin E., Kodyri R.S., Scimeca J.-C., Carle G., Gelb M.H.,
Lazdunski M., Lambeau G.;
"Cloning and recombinant expression of a novel mouse-secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shakhov A.N., Rubtsov A.V., Lyakhov I.G., Tumanov A.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION STRAIN=BALB/c;
                                                                                                                                                                                                                             144 AA
                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                   121 RNLDIYQKRLRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phospholipase A2.";
J. Biol. Chem. 274:19152-19160(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phospholipase A2s.";
J. Biol. Chem. 274:24973-24979(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6 X 129;
MEDLINE=21040292; PubMed=11196711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                                 PA2D MOUSE
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0; Gaps

Length 145;

99.3%;

Matches 144; Conservative

à

Local Similarity

Query Match

09 9

1 MELALLCGLVVWAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 1 MELALLCGLVVVMAGVIPIQGGILNLNKVVKQVTGKMPILSYMPYGCHCGLGGRGQPKDAT m

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RESULT 3
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                                     -!- FUNCTION: PAZ catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. L-alpha-1-palmitcyl-2-linoleoyl phosphatidylethanolamine is more efficiently hydrolyzed than the other phospholipids examined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
PRODOM; PB000303; PhospholipaseA2; 1.
SWART; SM00085; PA2c; 1.
PROSITE; PS00118; PA2 ASP; 1.
PROSITE; PS00118; PA2 HIS; 1.
Hydrolase; Lipid degradation; Signal; Calcium; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GROUP IID SECRETORY PHOSPHOLIPASE A2.
  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001),
                                                                                                                                                    acylglycerophosphocholine + a fatty acid anion.
--- COFACTOR: Binds 1 calcium ion per subunit.
--- SUBCELLULAR LOCATION: Secreted (isoform 1) and Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                      IsoId=09WVF6-2; Sequence=VSP 004508;
ISSUE SPECIFICITY: Expressed in several tissues including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.3%; Score 624.5; DB 1; Length 144; 71.0%; Pred. No. 3.8e-56; live 14; Mismatches 27; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTEN
CALCIUM (VIA CARBONYL OXYGEN)
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(BY SIMILARITY).
(BY SIMILARITY)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                          pancreas, spleen, thymus, skin, lung, and ovary. SIMILARITY: Belongs to the phospholipase A2 family.
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Missing (in isoform 2).
                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
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HSSP, P24605; ICLP.
MGD; MGI:1341796; P1a2g2d.
InterPro; IPR001211; PhospholipaseA2.
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EMBL, AF186824, AAF09019.1,
EMBL, AF169408, AAF42987.1,
EMBL, AF169408, AAF42988.1;
EMBL, AK018005, BAB31033.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF112983; AAD51391.1; -.
                                                                                                                                                                                                                         (isoform 2) (Potential).
-!- ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                          Name=2
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DISULFID
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60 DWCCQKHDCCYAHLKIDGCKSLTDNYKYSISQGTIQCSDNGSWCERQLCACDKEVALCLK 119
                                                                                                                                    DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
                                        MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=89350908; PubMed=2764915;
Ishizaki J., Ohara O., Nakamura E., Tamaki M., Ono T., Kanda A.,
Yoshida N., Teraoka H., Tojo H., Okamoto M.;
"CDNA cloning and sequence determination of rat membrane-associated phospholipase A2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
01-FBB-1991 (Rel. 17, Last sequence update)
11-PARA-2004 (Rel. 43, Last annotation update)
Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
(GIIC SPLA2).
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MEDLINE=88186890; PubMed=3356705;
MEDLINE=88186890; Ruranitsu S., Kagamiyama H., Okamoto M.;
Mon T., Tojo H., Kuramitsu S., Kagamiyama H., Okamoto M.;
"Purification and characterization of a membrane-associated phospholipase A2 from rat spleen. Its comparison with a cytosolic phospholipase A2 S-1.";
J. Biol. Chem. 263:5732-5738 (1988).
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"Structure of cDNA coding for rat platelet phospholipase A2.";
J. Biochem. 106:545-547(1989).
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"Structure of gene coding for rat group II phospholipase A2.";
Blochem. Blophye. Res. Commun. 168:1059-1065(1990).
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MEDLINE=90381322; PubMed=2400792;
Kusunoki C., Satch S., Kobayashi M., Niwa M.;
"Structure of genomic DNA for rat platelet phospholipase A2.";
Biochim. Biophys. Acta 1087:95-97(1990).
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STRAIN=Wistar: TISSUB=Platelet;
STRAIN=Wistar: TISSUB=Platelet;
SPEDIINE=89174508; PubMed=3235451;
Hayakawa M., Kudo I., Tomita M., Nojima S., Inoue K.;
"The primary structure of rat platelet phospholipase A2.";
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MEDLINE-90110043; PubMed=2606907;
                                                                                                                                                                                                                                                                                121 RNLDTYOKRLRFYWRPHCRGOTPGC 145
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                                                                                                                                                                                                                      Agreman A.J., de Jong J.G.N., Arnoldussen E., Neys F.W.,
Aarsman A.J., de Jong J.G.N., Arnoldussen E., Neys F.W.,
A medianar P.D., van den Bosch H.
A van Massenarar P.D., van den Bosch H.
Inmunoaffinity purification, partial sequence, and subcellular
localization of rat liver phospholipase A2.";
I. Calization of rat liver phospholipase A2.";
J. Biol. Chem. 264:10008-10014(1999).
J. FUNCTION: Thought to participate in the regulation of the phospholipid metabolism in biomembranes including eicosanoid phospholipid metabolism in biomembranes including eicosanoid biosynthesis: Catalyzes the calcium-dependent hydrolysis of the 2-
Diosynthesis: Catalyzes the calcium-dependent hydrolysis of the 2-
acyl groups in 3-an-phosphocylycerides.
C-: CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylglycerophosphocholine + a fatty acid anion.
C-: SUBCELLULAR LOCATION: Membrane-associated.
C-: SUBCELLULAR LOCATION: Membrane-associated.
C-: SUBCELLULAR LOCATION: Membrane-bound and secreted forms are identical and are encoded by a single gene.
C-: SIMILARITY: Belongs to the phospholipase A2 family.
                                                                 MEDLINE=888007474; PubMed=3654593; MEDLINE=888007474; PubMed=3654593; Hayakawa M., Horigome K., Kudo I., Tomita M., Nojima S., Inoue K.; "Amino acid composition and NH2-terminal amino acid sequence of rat platelet secretory phospholipase A2."; Jule 1900 10:1311-1314(1987).
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CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
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CALCIUM (VIA CARBONYL OXYGEN)
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PROSITE; PS00118; PA2_AIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
Hydrolase; Lipid degradation; Membrane; Signal; Calcium.
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CALCIUM (BY SIMILARITY).
P -> L (POLYMORPHISM).
S -> D (IN REF. 8).
W -> E (IN REF. 5).
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Pfam; PP00068; phoslip; 1.
PRINTS; PR00389; PHPHILPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
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HSSP; P14555; 1POD.
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                                                  TISSUE=Platelet;
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60 TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
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MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsiph F.,
Diatchenko L., Marusina K., Farmer Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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Kramer R.M., Johansen B., Hession C., Pepinsky R.B.;
"Structure and properties of a secretable phospholipase A2 from human
                                                                                                                                                                                                                                                                              1 MELALLCGIVVMA-GVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA
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Kramer R.M., Hession C., Johansen B., Hayes G., McGray P., Chow E.P.,
Tizard R., Pepinsky R.B.;
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01-JAN-1990 (Rel. 13, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-2004 (Rel. 43, Last annotation update)
Phospholipase A2, membrane associated precursor (BC 3.1.1.4)
(Phosphalidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
(GIIC SPLA2) (Non-ine Dancreatic secretory phospholipase A2) (NPS-PLA2),
PLA2G2A OR PLA2B OR RASF-A OR PLA2L.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-Rheumatoid arthritic synovial fluid;

MEDLINE=89174566; PubMed=2925608;

Seilhamer J.J., Pruzanski W. Vadas P., Plant S., Miller J.A.,

Kloss J., Johnson L.K.;

Kloss J., Johnson L.K.;

"Cloning and recombinant expression of phospholipase A2 present :rheumatoid arthritic synovial fluid.";
J. Biol. Chem. 264:5335-5338(1989).
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                                                                                                                                                                       DB 1; Length 146;
                                                                                                                                                                                                                               Indels
                                                                                                                     CRC64;
D -> E (IN REF. 5).
R -> S (IN REF. 5).
L -> V (IN REF. 3).
A -> S (IN REF. 5).
4; 60DDC9E79BF109F7 CR
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                                                                                                                                                                       46.9%; Score 399.5; DB
47.9%; Pred. No. 2e-33;
Live 23; Mismatches
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     69 D
78 R
85 L
121 A
16294 MW;
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Best Local Similarity 47.99
Matches 70; Conservative
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SEQUENCE FROM N.A.
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
Inman and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                          MEDLINE-89374261; PubMed=2775276;
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"The primary structure of a membrane-associated phospholipase A2 from
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 21-54.
TISSUB=Synovial fluid;
MEDLINE=89197814; Dubmed=3240982;
Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;
"Amino acid composition and NH2-terminal amino acid sequence of human phospholipase A2 purified from rheumatoid synovial fluid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=95393225; PubMed=7664108;
Schevitz R.W., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K.,
Dillard R.D., Draheim S.E., Hartley L.W., Jones N.D., Mihelich E.D.,
Olkowski J.L., Snyder D.W., Dand S.C., Wery J.-P.;
"Structure-based design of the first potent and selective inhibitor
of human non-pancreatic secretory phospholipase A2.";
Nat. Struct. Biol. 2:458-465(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.; "Purification and characterization of a phospholipase A2 from human ileal mucosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91287826, PubMed=2062381,
Wery U.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
Wery U.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,
Gamboa G., Goodson T. Jr., Hermann R.B., Kramer R.M., McClure D.B.,
Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,
"Structure of recombinant human rheumatoid arthritic synovial fluid
Nature 352:79-82(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lai C.Y., Wada K.; "Phospholipase A2 from human synovial fluid: purification and structural homology to the placental enzyme."; Biochem. Biophys. Res. Commun. 157:488-493 (1988).
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Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,
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TISSUE-Synovial fluid;
MEDLINE-89976274; PubMed-3202859;
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TISSUE=Ileal mucosa;
MEDLINE=94002200; PubMed=8399335;
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Science 254:1007-1010(1991).
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       MEDLINE=98207049; PubMed=953825;

A Kitadokoro K., Hagishita S., Sato T., Ohtan M., Miki K.;

Kitadokoro K., Hagishita S., Sato T., Ohtan M., Miki K.;

T "Crystal structure of human secretory phospholipase A2-IIA complex

T "Tystal structure of human secretory phospholipase A2-IIA complex

T "Tystal structure of human secretory phospholipase A2-IIA complex

T "Tystal structure of human secretory phospholipase A2-IIA complex

T "Tystal structure of human secretory phospholipase A2-IIA complex

T "Tystal structure of human secretory phospholipase A2 is found in many cells

T "Subcartors binds I calcium ion per subunit.

C -: COFACTOR: Binds I calcium ion per subunit.

C -: SURELLANEOUS: Group II phospholipase A2 is found in many cells

and also extracellularly. The membrane-bound and secreted forms

C -- SIMILARITY: Belongs to the phospholipase A2 family.
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(VIA CARBONYL OXYGEN).
(VIA CARBONYL OXYGEN).
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InterPro: IPR001211; PhospholipaseA2.
Fam, PP00068; Phoslip; I.
PRINTS: PR00189; PHPHLIPASEA2.
PLODOM, PD00303; PhospholipaseA2; 1.
SMART; SM00085; PA2C; 1.
PROSITE; PS00118; PA2 H1S; 1.
PROSITE; PS00118; PA2 HS; 1.
Hydrolase; Lipid degradation; Membrane; Signal; Calcium;
   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
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EMBL; M22431; AAA36549.1; -.
EMBL; BC005919; AAH05919.1; -.
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PDB; 1DCY; 12-NOV-99.
Genew; HGNC:9031; PLA2G2A.
MIM; 172411; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1POD; 31-OCT-93.
PDB; 1POE; 31-OCT-93.
PDB; 1KVO; 07-JUL-97.
PDB; 1DB4; 12-NOV-99.
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1BBC; 31-OCT-93.
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PRINTS; PR00389; PHPHLIPASEA2
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"Expression of the type-II phospholipase A2 in alveolar macrophages."

"Expression of the an inflammatory signal.";

"Expression of the phospholipal metabolism in biomembranes including eloosanoid phospholipid metabolism in biomembranes including eloosanoid biosynthesis (By similarity). Catalyzes the calcium-dependent bydrolysis of the 2-acyl groups in 3-sn-phosphogyycerides.

"CATALYTIC ACTIVITY: Phosphatidylcholine + H(12)0 = 1-
acylglycerophosphocholine + a fatty acid anion."

"COPACTOR: Binds 1 calcium ion per subunit (By similarity).

"COPACTOR: Binds 1 calcium mon per subunit (By similarity).

"INSUE SPECIFICITY: Alveolar macrophages, and at much lower levels in peripheral blood monocytes and peritoneal macrophages."

"INSUE SPECIFICITY: Belongs to the phospholipase A2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                               DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
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FMRR-2004 (Rel. 43, Last annotation update)
Phospholipase A2, membrane associated precursor (BC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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                                                                                                         DB 1; Length 144;
                                                                                                      46.4%; Score 395.5; DB 1; Length 47.6%; Pred. No. 4.9e-33; tive 23; Mismatches 52; Indels
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or send an email to license@isb-sib.ch).
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HSSP, P14555; 1POD.
InterPro; 1PR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
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STRAIN=Hartley; TISSUE=Macrophage;
MEDLINE=95340522; PubMed=7615534;
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MEDLINE=95403435; PubMed=7673223.

KENNEDS 95403435; PubMed=7673223.

Kennedy B.P., Payette P., Mudgett J., Vadas P., Pruzanski W.,
Ywan M., Tang C., Rancourt D.E., Cromlish W.;

Ywan M., Tang C., Rancourt D.E., Cromlish W.;

In inbred mouse strains.";

J. Biol. Chem. 270:22378-22385(1995).
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Phospholipase A2, membrane associated precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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49.3%; Pred. No. 2.2e-32;
ive 20; Mismatches 52; Indels
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         ProDom; PD000303; PhospholipaseA2; 1.
SMRT; SM00085; PA2c; 1.
PROSITE; PS00118; PA2_HIS; 1.
PROSITE; PS00119; PA2_ASP; 1.
Hydrolase; Lipid degradation; Membrane; Signal; Calcium. SIGNAL
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68 CALCIUM (BY SIMILARITY).
16153 MW, 13F22C96594D304D CRC64;
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P31482; Q60871;
01-JUL-1993 (Rel. 26, Created)
". Arm-2003 (Rel. 42, Last sequence update)
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                                                                                                                                                           MEDLINE-22388557; PubbMed=12477932;

MEDLINE-22388557; PubbMed=12477932;

MINIBEACTARETAN, Feingold E.A., Grouse L.H., Derge J.G.,

Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausberg R.L., Seeberg B., Wagner L., Sheamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Datchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,

Datchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Salaka U., Smailus D.E.,

Bohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 22-146 FROM N.A. STRANTB-BALBACT TISSUE-Small intestine;
STRANTB-BALBACT TISSUE-Small intestine;
Mulherkar R., Ro. R.S., Wagle A.S., Patki V., Deo M.G.;
"Enhancing factor, a Paneth cell specific protein from mouse small intestines: predicted amino acid sequence from RT-PCR amplified cDNA and its expression.";
Biochem. Biophys. Res. Commun. 195:1254-1263(1993).
                          MEDLINE=95300227; PubMed=7781071;
MacPhee M., Chepenik K.P., Liddell R.A., Nelson K.K., Siracusa L.D.,
                                                                       "The secretory phospholipase A2 gene is a candidate for the Moml locus, a major modifier of ApcMin-induced intestinal neoplasia."; Cell 81:957-966(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94071967; PubMed=8250944;
Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;
Biochem. Biophys. Res. Commun. 197:351-352(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY SEQUENCE OF 22-41.
                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences.
SEQUENCE FROM N.A.
                                                          Buchberg A.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00085; PAZC; I...FROSTE; SM00085; PAZC; I...FROSTE; PS00118; PAZ HIS; 1. PROSITE; PS00119; PAZ-ASP; 1. Hydrolase; Lipid degradation; Calcium; Growth regulation; Signal; Membrane; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 43.6%; Score 371.5; DB 1; Length 146; 1 Similarity 47.3%; Pred. No. 1.3e-30; 69; Conservative 19; Mismatches 57; Indels 1.
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CALCIUM (VIA CARBONYL OXYGEN)

(BY SIMILARITY).

CALCIUM (VIA CARBONYL OXYGEN)
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(BY SIMILARITY).
69 CALCIUM (BY SIMILARITY).
19 V -> D (IN REF. 1).
86 K -> T (IN REF. 1).
16145 MW, AB904F6B3BIBA5C7 CRC64;
-!- SIMILARITY: Belongs to the phospholipase A2 family.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P1455; 1POD.
MGD; MGI:104642; P1a2g2a.
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip, P.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                               EMBL; X74266; CAA52325.1; -.
EMBL; U32358; AAC5225.1; -.
EMBL; U28344; AAB06315.1; ALT_INIT.
EMBL; BC045156; AAH45156.1; -.
PIR; 148342; 148342.
PIR; S29495; S29495.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted. Trissus SPECIFICATION: Secreted. Trissus SPECIFICITY: Expressed at high levels in placenta, testis, thymus and at lower levels in heart, kidney, liver and prostate. SIMILARITY: Belongs to the phospholipase A2 family.
broup IIF secretory phospholipase A2 precursor (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase GIIF) (GIIF spLA2) (spLA(2)-IIF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the acyl groups in 3-sn-phosphoglycerides. Hydrolyzes phosphatidylglycerol versus phosphatidylcholine with a 15-fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTENTIAL).
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                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=20563827; PubMed=11112443;
Valentin E., Singer A.G., Ghomashchi F., Lazdunski M., Gelb M.H.,
                                                                                                                                                                                                                                                                                                                                              "Cloning and recombinant expression of human group IIF-secreted phospholipase A(2)."; Biochem. Biophys. Res. Commun. 279:223-228(2000).
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CALCIUM (VIA CARBONYL OXYGEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-acylglycerophosphocholine + a fatty acid anion. COFACTOR: Binds 1 calcium ion per subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wallis J.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF306566; AAG50242.1; -.
EMBL; AL158172; CAC13160.1; ALT_INIT.
HSSP; P82287; 10HL.
HSSP; P82287; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0004623; F:phospholipase A2 activity; NAS.
InterPro; IPR001211; PhospholipaseA2.
FRIMTS; PR00089; PHPHLIPASEA2.
PRODM; PR000309; PHPHLIPASEA2.
ProDom; P0000309; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
PROSITE; PS00119; PA2_ASP; FALSE_NEG.
PROSITE; PS00119; PA2_ASP; FALSE_NEG.
PROSITE; PS00118; PA2_HIS; 1.
Hydrolase; Lipid degradation; Signal; Calcium.
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CALCIUM (VIA CA
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                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                            Lambeau G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C. Submittee of (OCT-2000) to the EMBL/GenBank/DDBJ databases.

C. Submittee of (OCT-2000) to the EMBL/GenBank/DDBJ databases.

C. FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-catalyzes the calcium-dependent hydrolyzes

C. Stroups in 3-sn-phosphoslycerides. This is sozyme hydrolyzes

more efficiently L-alpha-1-palmitoyl-2-oleoyl phosphatidylcholine, L-catalyzer-1-palmitoyl-2-arachidonyl phosphatidylcholine, L-calpha-1-stearcyl-2-arachidonyl phosphatidylinositol. May be involved in the production of lung surfactant, the remodeling or regulation of cardiac muscle.

C. TATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-catalyger-ophosphocholine + a fatty acid anion.

C. COFACTOR: Binds 1 calcium ion per subunit (By similarity).

C. SUBCELLULAR LOCATION: Secreted.

C. SUBCELLULAR LOCATION: Secreted.

C. TISSUE SPECIFICITY: Heart, placenta and less abundantly, in lung.

C. PIM: This enzyme lacks one of the seven disulfide bonds found in
                                                                                                                                                                                                                             63 CCQTHDCCYDHLKTQGCGIYKDYYRYNFSQG-NIHCSD-KGSWCEQQLCACDKEVAFCLK 120
                                                                                                                                                                                                                                                        63 CCHAHDCCYQELFDQGCHPYVDHYDHIENNTEIVCSDLNKTECDKQTCMCDKNWVLCLM 122
                                                                                                                                                                      3 LALICGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Calcium-dependent phospholipase A2 precursor (EC 3.1.1.4)
(Phosphatidylcholine 2-acylhydrolase) (PLA2-10) (Group V phospholipase
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB=Stomach;
MEDILINE=94131989; PubMed=8300559;
Chen J., Engle S.J., Scilhamer J.J., Tischfield J.A.;
Chen J., Bngle S.J., Scilhamer J.J., Tischfield J.A.;
"Cloning and recombinant expression of a novel human low molecular weight Ca(2+)-dependent phospholipase A2.";
J. Biol. Chem. 269:2365-2368 [1994].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similar PA2 proteins.
--- miscellanboods: Maximal activity is found at pH 6.5 and remains high up to pH 9.0.
--- SIMILARITY: Belongs to the phospholipase A2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;
                                                                                                     ..
                                                         Length 168;
                                                                                                     Indels
                   35B159298246A762 CRC64;
CALCIUM (BY SIMILARITY)
                            41.3%; Score 352; DB 1; De 45.5%; Pred. No. 1.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 AA
                                                                                                                                                                                                                                                                                                                   121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                                                                                                                                                           123 N--QTYREEYRGFLNVYCQGPTPNC 145
                   18658 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 31, Created)
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                     168 AA;
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
  68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995
                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA25 HUMAN
P39877;
                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wallis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLA2G5
    METAL
                                                                                                         Matches
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Local Similarity
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                                                                                 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PA22 BOTMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9I834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA22 BOTMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DWCCWAHDHCYGRLEEKGCNIRTQSYKXRFAWGVVTC-EPGFPCHVNLCACDRKLVYCLK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                      . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       12 MAGVIP------IQGGILNLNNAVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                          R Mim; 601192; ...
R GO; GO:0005576; C:extracellular; TAS.
GO; GO:0005576; C:extracellular; TAS.
GO; GO:0006445; P:calcium-dependent secreted phospholipase A2. ..;
R GO; GO:0006644; P:phospholipid metabolism; TAS.
R InterPro; IPR001211; PhospholipaseA2.
R PRINTS; PR0068; phoslip; 1.
R PRINTS; PR00189; PhPHLIPASEA2.
R ProDom; PR00019; PA2. 1.
R PROSTIE; PS00119; PA2. HIS; 1.
R PROSTIE; PS00119; PA2. ASP; 1.
R Hydrolase; Lipid degradation; Calcium; Signal.
SIGNAL
                                                                                                                                                                                                 COLGINA DEPENDENT PHOSPHOLIPASE A2.
BY SIMILARITY.
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(CALCIUM (BY SIMILARITY).
(CALCIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pescatori M., Grasso A., Rufini S.;
"Molecular cloning of a K-49 PLA2-like myotoxin from the snake
Bothrops asper.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospholipase A2 homolog 3 precursor (Myotoxin III) (MI-3-3).
                                                                                                                                                                                                                                                                                                                                                                                                  Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                     36; Indels
                                                                                                                                                                                                                                                                                                                                                                                             40.7%; Score 347; DB 1;
43.6%; Pred. No. 3.7e-28;
iive 27; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
        EMBL; U03090; AAC28886.1; -.
EMBL; AL158172; CAC13158.1; -.
PIR; A49959; A49959; HSSP; P14421; 1A2A.
                                                                                                                                                                                                                                                                                                                                                                           15674 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bothrops asper (Terciopelo)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNLDTYOKRLRFY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||| :| :::
120 RNLRSYNPQYQYF 132
                                               Genew, HGNC:9038; PLA2G5
                                                                                                                                                                                                                                                                                                                                                                                                                   58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                             64
1117
1103
103
                                                                                                                                                                                                                                                                                                                      49
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 58: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                         138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           21
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ACT_SITE
DISULFID
DISULFID
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Ruropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 CYK--KLTGCNPKKDRYSYSWKDKTIVCGENNS-CLKELCECDKAVAICLRKNLDTYNKK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                        -!- MISCELLANEOUS: Does not bind calcium as one of the calcium binding ligands is lost (Asp->Lys in position 64) (Probable).
-!- SIMILARITY: Belongs to the phospholipase A2 family. Group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
Viperidae, Crotalinae, Bothrops.
                            -!- FUNCTION: Myotoxic protein that lacks enzymatic activity (By
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C.

EMBL; AR109911; AAR14241.1; -..

DR EMBL; PR00068; phospholipaseA2.

DR PRINTS; PR00389; PHPHLIPASEA2.

DR PRANT; SR00189; PPHLIPASEA2.

DR SMART; SR0019; PA2 ASP; 1.

DR SMART; SR00118; PA2 ASP; 1.

DR SMART; SR00118; PA2 ASP; 1.

DR PROSITE; PS00118; PA2 ASP; 1.

DR SMART; SITE | PR0118; PA2 ASP; 1.

DR SMART; SITE | PR0118; PA2 ASP; 1.

TOXIN; Signal; Multigene family.

FT SIGNAL

TOXIN; Signal; Multigene family.

TOXIN; Signal; Multigenery.

TOX
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospholipase A2 homolog 2 (Myotoxin II) (MjTX-II) (M-VI).
Bothrops moojeni (Lance-headed viper) (Caissaca).
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                        -!- SUBCELLULÂR LOCATION: Secreted (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.0%; Score 340.5; DB 1
47.4%; Pred. No. 1.7e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-52, AND CHARACTERIZATION.
TISSUE-Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 YKNNYLKPFCKKADP 137
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us-09-830-321a-1.rsp

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141 QTP
                                                                                                                                                                                                    28-FEB-2003
10-OCT-2003
                                                                                                                                            PA2F MOUSE
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzymes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT SITE
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                                                                                                                                                                                                                                                                                  PLA2G2F
                                                                                                                                                          Q9QZT4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                          PA2F_MOUSE
                                                                                                                                                                g
            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ъ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLUIAR LOCATION: Secreted.
MISCELLUIAR LOCATION: Secreted.
MISCELLANEOUS: Does not bind calcium as one of the calcium binding anscens is lost (Asp.-Lys in position 48).
SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ILNINKMYKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFBLGKMILQETCKNPAKSYGVYGCNCGVGGRGKPKDATDRCCYVHKCCYK--KLTGCDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                    de Azevedo W.F., Ward R.J., Lombardi F.R., Giglio J.R., Soares A.M., Fontes M.R.M., Arni R.K.; "Crystal structure of myotoxin-II: a myotoxic phospholipase A2 homologue from Bothrops moojeni venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                         Lacks
                                                                                                                                                                          TISSUE=Venom gland;
Soares A.M., Ward R.J., Rodrigues-Simioni L., Lomonte B.,
Gutierrez J.M., Guerra-Sa R., Rodrigues V., Fontes M.R.M., Arni R.K.
        Soares A.M., Rodrigues V.M., Homei-Brandeburgo M.I., Toyama M.H., Lombardi F.R., Arni R.K., Giglio J.R.;

"A rapid procedure for the isolation of the Lys-49 myotoxin II from Bothrops moojeni (caissaca) venom: biochemical characterization, crystallization, myotoxic and edematogenic activity.";

Toxicon 36:503-514(1998).
                                                                                                                                                                                                                                                                                                                                                                                             Protein Pept. Lett. 4:329-334(1997).

--- FUNCTION: Displays myotoxin and edema-inducing activities. Lacks PA2 enzymatic activity as well as of hemorrhagic, anticoagulant and coagulant activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
W. 120A53FAB3009CB CRC64;
                                                                                                                                                                                                                                                Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.4%; Score 336; DB 1; 50.4%; Pred. No. 4.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF145759; AAF66702.1; -.
HSSP, P82287; 1QLL.
InterPro: IPR001211; PhospholipaseA2.
Pfam, PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
PROSITE; PS00119; PA2. ASP; 1.
PROSITE; PS00118; PA2. ASP; 1.
PROSITE; PS00118; PA2. ASP; 1.
TOAIN; Multigene family.
MEDLINE=98299483; PubMed=9637370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13887 MW;
                                                                                                                                                        SEQUENCE OF 15-122 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
95
122
88
81
86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY.
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75
18
122 AA;
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Best Local Similarity
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28
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                                                                                                                                                                                                                                                                                                              TISSUE=Venom;
                                                                                                                                                                                                                                    Giglio J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                   Group IIF secretory phospholipase A2 precursor (BC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase GIIF) (GIIF sPLA2) (sPLA(2)-IIF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 274:31195-31202(1999).
FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acyl groups in 3-sn-phosphoglycerides. Hydrolyzes phosphatidylglycerol versus phosphatidylcholine with a 15-fold preference (By similarity).

-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-acylglycerophosphocholine + a fatty acid anion.

-!- CORACTOR: Binds 1 calcium ion per subunit.

-!- SUBCELLULAR LOCATON: Secreted.

-!- SUBCELLULAR LOCATON: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
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GROUP IIF SECRETORY PHOSPHOLIPASE A2.
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20002639; PubMed=10531313; Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.; Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.; "On the diversity of secreted phospholipases A2. Cloning, tissue distribution, and functional expression of two novel mouse group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALCIUM (VIA CARBONYL OXYGEN)
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InterPro; IPR001211; PhospholipaseA2.
InterPro; IPR001211; PhospholipaseA2.
Pfam; PR00068; phoslib; 1.
PRINTS; PR003089; PHPHLIPASEA2.
PROOM; PD000303; PhospholipaseA2; 1.
PROSITE; PS00119; PA2_ASP; FALSE_NEG.
PROSITE; PS00119; PA2_ASP; FALSE_NEG.
PROSITE; PS00119; PA2_HIS; 1.
Hydrolase; Lipid degradation; Signal;
                                                                                                                                                                                                                                                       (Rel. 41, Last sequence update) (Rel. 42, Last annotation update)
                                                                                                                                                                           168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF166099; AAF04500.2; -.
HSSP; P00593; 4BP2.
                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
1138
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1113
1111
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144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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(BY SIMILARITY).

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DISULFID
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                                                                                                                                                        63 CCQTHDCCYDHLKTQGGGIYKDYYRYNFSQGN-IHCSD-KGSWCEQQLCACDKEVAFCLK 120
                                                                                                                        62
                                                                                                                             3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES=C.d.terrificus; TISSUE=Venom gland;
MEDLINE=89016587; PubMed=3174444;
Ducancel F., Guignery Frelat G., Menez A., Boulain J.-C., Bouchier C.,
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=C.d.terrificus;
MEDLINE=86321988; PubMed=3753003;
Aird S.D., Kaiser I.L., Lewis R.V., Kruggel W.G.;
Aird S.D., acomplete amino acid sequence for the basic subunit of crotoxin.";
Arch. Blochem. Blophys. 249:296-300
                                                                                                                                                                                                                                                                                                                                (Crotoxin basic chain 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          basic subunits of Mojave non-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=C.S.scutulatus; TISSUE=Venom; MEDLINE=20385490; PubMed=2402763; Aird S.D., Kruggel W.G., Kaiser II.; Medica acid sequence of the basic subunit of Mojave toxin from the venom of the Mojave rattlesnake (Crotalus s. scutulatus)."; Toxicon 28:669-673(1990).
                                                                                                                                                                                                                                                                                                                                                                    Crotalus scutulatus scutulatus (Mojave ratilesnake)

Wararyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Crotalus.
                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                          Crotalus durissus terrificus (South American rattlesnake), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and sequencing of cDNAs encoding the two subunits of
                                                                       39.4%; Score 336; DB 1; Length 168; ilarity 42.8%; Pred. No. 5.8e-27; Conservative 23; Mismatches 52; Indels
   CALCIUM (VIA CARBONYL OXYGEN)
            (BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
                                                                                                                                                                                                                                                                                 P07517; P23559;
01-APR-1988 (Rel. 07, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Phospholipase A2 CB1 precursor (EC 3.1.1.4) (Crotoxin basic (Mojave toxin basic chain) (Mtx-b) (Phosphatidylcholine 2-
                              (BY SIMILARITY).
CALCIUM (BY SIMILARITY).
9E15FB6AC0F5450C CRC64;
                                                                                                                                                                                                                                                                            138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES C. s. scuttlatus; TISSUE-Liver; MEDLINE=94156205; PubMed=8112610; John T.R., Smith L.A., Kaiser I.I.; Genomic sequences encoding the acidic and toxin: unusually high sequence identity of Gene 139:229-234(1994).
                                                                                                                                                                                                  121 RNLDTYOKRLRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                               : |: | |: | | | DH--PYRNKYRGYFNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 16:9050-9050(1988).
                                                                                                                                                                                                                                                                            PRT;
                                                    18880 MW;
                                                                                                                                                                                                                                                                           STANDARD;
  49
                       51
                                          68
168 AA;
                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
  49
                     51
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                                                   SEQUENCE
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 METAL
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**MEDLINE==04307256; PubMed=9033899;
**RA MEDLINE=94307256; PubMed=8033899;
**RA MEDLINE=94307256; PubMed=8033899;
**RA MEDLINE=94307256; PubMed=8033899;
**RA Monegier B., Vuilhorgne M., Bon C.;
**RA Monegier B., Vuilhorgne M., Bon C.;
**RT "The origin of the diversity of crotoxin isoforms in the venom of Crotalus durissus terrificus.";
**R. Eur. J. Biochem. 223.161-164(1994).
**C. "InvicTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-cayl groups in 3-sn-phosphoglycerides. Inhibits neuromuscular cransmission by blocking acetylcholine release from the nerve cc transmission by blocking acetylcholine + H(2)0 = 1-caylglycerophosphocholine + a fatty acid anion.
**C. "CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-copacing supplycerophosphocholine + a fatty acid anion.
**C. "COPACIONE Binds I calcium ion per subunit (By similarity).
**C. "COPACIONE. Binds I calcium ion per subunits: acidic and basic.
**The acidic subunit is nontoxic, without enzymatic activity and is comprises 3 peptides that are crosslinked by 7 disulfide bridges.
**C. "Comprises 3 peptides that are crosslinked by 7 disulfide bridges.
**C. "Comprises 3 peptides that are crosslinked by 7 disulfide bridges.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           composed of a single chain.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the venom gland.
SIMILARITY: Belongs to the phospholipase A2 family. Group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY)
(BY SIMILARITY)
(BY SIMILARITY)
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(BY SIMILARITY)
(BY SIMILARITY)
(CALCIUM (VIA CARBONYL OXYGEN)
(CALCIUM (VIA CARBONYL OXYGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Presynaptic neurotoxin; Calcium; Signal; Multigene family. SIGNAL
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84A118931DFFE2E3 CRC64;
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Pfam; PF00068; phoslip; 1
PRINTS; PR00389; PHPHLIPASEA2.
Propom; PD003303; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
PROSITE; PS00119; PA2 ASp; 1.
PROSITE; PS00119; PA2 AIS; 1.
PROSITE; PS00119; PA2 AIS; 1.
PROSITE; PS00118; PA2 AIS; 1.
PROSITE; PS00118; PA2 AIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHOLIPASE A2
SPECIES=C.d.terrificus; TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X12603; CAA31123.1; -. EMBL; U01027; AAC59674.1; -.
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PIR; S02257; PSRSBT.
HSSP; P14421; 1A2A.
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DISULFID
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subfamily.
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Best Local
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                                 70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
                                              66 CYG--KLAKCNIKWDIYPYSLKSGXITCG-KGTWCEEQICECDRVAARCLRRSLSTYKYG 122
TISSUE=Venom gland;
MEDLINE=92409555; PubMed=1528861;
Ogawa T., Oda N., Nakashima K.-I., Sasaki H., Hattori M., Sakaki Y.,
                                                                                                                                                                                                                                                                                                                                          Tithara H., Ohno M.;

"Unnsually high conservation of untranslated sequences in cDNAs for Trinnersurus flavoviridis phospholipase A2 isozymes.";

Trinnersurus flavoviridis phospholipase A2 isozymes.";

Proc. Natl. Acad. Sci. U.S.A. 89:8557-8561(1992).

-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the
                                                                                                                                                                        01-FBB-1994 (Rel. 28, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
01-FBB-1994 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phospholipase AZ isozyme PL-X' precursor (EC 3.1.1.4)
(Phospholipase AZ isozyme PL-X' precursor (EC 3.1.1.4)
(Phospholipase AZ isozyme PL-X' precursor (EC 3.1.1.4)
Trimeresurus flavoviridis (Habu).
Trimeresurus flavoviridis (Habu).
Lepidosauria; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR01211; PhospholipaseA2.
InterPro; IPR01211; PhospholipaseA2.
PRINTS; PR00308; phoslip; 1.
PRONO08; PR00030; PhospholipaseA2; 1.
SWART; SW00085; PA2c; 1.
PR0STIE; PS001119; PA2 A8P; 1.
PR0STIE; PS00118; PA2 HIS; 1.
Hydrolase; Lipid degrādation; Calcium; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHOLIPASE A2 ISOZYME PL-X'.
                                                                                                                                                                                                                                                                                                                                                                                            2-acyl groups in 3-sn-phosphoglycerides.
CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
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SIMILARITY.
SIMILARITY.
SIMILARITY.
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                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D10721; BAA01564.1; -. HSSP; P51972; 1VAP.
                                                                                                     123 YMFYPDSRCRGPSETC
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105
1131
1111
1138
104
                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           NCBI TaxID=88087;
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444
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CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
acylglycerophosphocholine + a fatty acid anion.

COPACTOR: Binds 1 calcium ion per subunit (By similarity).

COPACTOR: Binds 1 calcium ion per subunit s: CA and CB. CA is acidic, subunits: Crotoxin consists of 2 subunits: CA and CB. CA is acidic, nontoxic, without enzymatic activity and comprises 3 peptides that are crosslinked by 7 disulfide bridges. CB is basic, toxic, has phospholipase A2 activity and is composed of a single chain.

SUBCELLUIAR LOCATION: Secreted.

SINGELLUIAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                 9 VLLVGV---EGHLLQFRKMIKKMTGKEPIVSYAFYGCYCGKGGRGKFKDATDRCCFVHDC
                                                                                                                                                                                                                                                                                                          Gaps
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01-MAR-1992 (Rel. 21, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-oCT-2003 (Rel. 42) Last annotation and the sequence (Phospholine 2-acylhydrolase).
11-oCT-2003 (Rel. 42) Creating Couth American rattlesnake)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEGURNCE FROM N.A.
TISSUE-Venom gland;
MEDLINE-91198145; PubMed=2015302;
MEDLINE-91198145; PubMed=2015302;
MEDLINE-91198145; PubMed=2015302;
"Analysis of CDNAs encoding the two subunits of crotoxin, a phospholipase A2 neurotoxin from rattlesnake venom: the acidic non phospholipase A2 neurotoxin from a phospholipase A2-like precursor.";
Biochim. Biophys. Acta 1088:401-408(1991).
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                                                                                                                                                                                                                                                    Length 138;
                                                                                                               CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (BY SIMILARITY).
471B01878CCA1ED1 CRC64;
                                     (BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
                  (VIA CARBONYL OXYGEN)
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1 Similarity 46.3%; Pred. No. 1.2e-26;
63; Conservative 19; Mismatches 48; Indels
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SIMILARITY.
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102
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123 FRYHLKPSCKKTSEQC 138
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phospholipase A2 howolog Dac-K49II precursor.
Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Viperidae; Crotalinae; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                     EMBL; X16100; CAA34227.1; --
PIR; S15068; PSRSB2.
InterPro: 12801211; PhospholipaseA2.
Ffam; PF00068; phoslip; 1.
Prom; PF00068; phoslip; 1.
ProDom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2; 1.
SMART; SM00085; PA2; 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS00118; PA2_HIS; 1.
Hydrolase; Lipid degradation; Calcium; Signal; Multigene family.
SIGNAL
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CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
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44.1%; Pred. No. 1.3e-26;
tive 21; Mismatches 52; Indels
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935D12258D47B058 CRC64;
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Matches 60; Conserv
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TISSUE=Venom gland;
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                                                                                                                                                                                                                                                                                                                                     -- FUNCTION: Myotoxic protein that lacks PA2 enzymatic activity.
-- SUBCELLULAR LOCATION: Secreted (By similarity).
-- TISSUE SPECIFICITY: Expressed by the venom gland.
-- MISCELLANBOUS: Does not bind calcium as one of the calcium binding ligands is lost (Asp->Lys in position 64).
-- SIMILARITY: Belongs to the phospholipase A2 family. Group II
                                                                                                                                                                                                                                                         novel Lys-49
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                           Fan C.Y., Qian Y.C., Yang S.L., Gong Y.;
                                                                                                                                                                   TISSUE=Venom gland;
MINDLIMES-1478855; PubMed=11594738;
Tsai I.-H. Chen Y.-H., Wang Y.-M., Tu M.-C., Tu A.T.;
"Purification, sequencing, and phylogenetic analyses of novel lysphospholipases A(2) from the venoms of rattlesnakes and other pit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHOLIPASE A2 HOMOLOG DAC-K49II.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
S -> L (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.8%; Score 330.5; DB 1
43.4%; Pred. No. 1.7e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Mismatches
                                                                                                                                                                                                                                                                                                                 Arch. Biochem. Biophys. 394:236-244(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1MC2; 21.4UG-02.
PDB; 1MC6; 04-SEP-02.
InterPor: IPR001211; PhospholipaseA2.
Pfam; PF000068; phoslip; 1.
PRINTS; PR00389; PHPHIJPASEA2.
ProDom; PD00033; PhospholipaseA2; 1.
SWART; SW00018; PA2.; 1.
PROSITE; PS00119; PA2. ASP; 1.
TOXIN; Signal; 30-structure.
3.IGNAL.
1. 16 BY SIMILARI
WEDLINE=99183869; PubMed=10084123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ223188; CAA11159.1; -. EMBL; AF269132; AAL36975.1; -.
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                                                                                                       Genet. Anal. 15:15-18(1999)
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Best Local Similarity 43.4<sup>1</sup>
Matches 59; Conservative
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138 AA;
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us-09-830-321a-1.rsp

Search completed: October 5, 2004, 19:25:30 Job time : 6.8 secs

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O91y34 rattus norv
O9qx68 mesocricetu
Q8n217 homo sapien
Q8n435 homo sapien
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Q804d7 bothrops ja
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vipera russ
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                                                       ; Search time 28.8067 Seconds (without alignments) 1588.179 Million cell updates/sec
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1 MELALLCGLVVMAGVIPIQG......YQXRLRFYWRPHCRGQTPGC 145
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Q805a2
Q7t1d5
Q8k0y1
Q7zzq1
Q8axy1
Q7t1c6
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Q805a3
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                1017041 seqs, 315518202 residues
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                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     - protein search, using sw model
                                                        October 5, 2004, 18:51:24
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Q8CE14
Q804D7
Q8BJ93
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Q9QX68
Q8N217
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Q7T3S7
Q805A2
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Q8K0Y1
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Q7T1C6
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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sp_vertebrate:*
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1: sp_archea:*
2: sp_bacteria:*
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Perfect score:
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312.5
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07T1D1	Q7T1D4	Q7T1D3	Q7T1D2	Q800C2	Q800C4	Q800C1	O7ZTA7	Q800C3	Q8C5Y6	Q7T3T5	Q7ZTA8	Q7ZTA6	Q7ZW60	Q7T2Q5	Q8WS8B	Q7T2Q4	Q7T1R0	080211	Q80ZM2	Q8AXW2	Q8K130	QBAXWO	Q9YH62	057313	Q86DU7	OBIMLO	O8AXW7	Q8AY48	
13	13	13	13	13	13	13	13	13	11	13	13	13	13	m	'n	m	13	13	11	13	11	13	13	13		'n	~	13	
138	138	138	138	138	138	138	138	138	141	130	138	138	147	147	156	147	146	142	453	146	144	145	149	149	167	177		137	
32.2	31.6		31.6			。	30.5		ö	29.5	œ	æ	7	26.1	26.0	S.	24.7	24.4	ω,	23.3		3	Э.	'n	۲,	22.5	ά.	ς.	
274.5	269.5	269.5	269.5	261.5	260.5	260.5	259.5	255.5	255.5	251.5	246	4	234	222.5	221.5	218.5	210.5	208		98	97	196.5	196	196	192.5	192	189.5	æ	
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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1. SEQUENCE FROM N.A.

1. SEQUENCE FROM N.A.

1. SEGUENCE FROM N.A.

1. SEGUENCE FROM N.A.

1. SEQUENCE TO STRAIN=Wistar; TISSUB=Blood;

1. A. Liu T.T., Liang N.S., Meng Z.Q., Xie Y.A., Kuang Z.P., Li Y.;

1. Tom whole blood.";

1. Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

2. Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

3. Rebl. AF165363; AAKS2061.1; -..

3. Rebl. AF165363; Fishospholipase A2 activity; IEA.

4. GO; GO:0006623; F:lpid catabolism; IEA.

5. GO; GO:00166422; F:lpid catabolism; IEA.

6. GO; GO:00166421; PhospholipaseA2.

6. BEAMY: PRO0068; phoslip; 1.

6. DR PRINTS; PRO0039; PHPHLIPASEA2.

6. PRODOM; PD000303; PhospholipaseA2; 1.
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.0%; Score 400.5; DB 11; Length 146; 47.9%; Pred. No. 3e-38; Live 23; Mismatches 52; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
PLATELET PHOSPHOLIPASE A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16306 MW; 60C1C9EC85DCBD67 CRC64;
                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Platelet phospholipase A2 precursor (Fragment)
                                        146 AA.
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00085; PA2C; 1.
PROSITE; PS00119; PA2 ASP; 1.
PROSITE; PS00118; PA2 HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47.9
Matches 70; Conservative
                                      PRELIMINARY;
                                                                                                                                              Rattus norvegicus (Rat).
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>146
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SEQUENCE
                                                   Q91Y34;
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SIGNAL
                                    Q91Y34
RESULT 1
                      091Y34
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Gaps

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124 QKSYSWKYLMGIKKSCEGESPSC 146
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Rh May P. 14551361; Cab62564.1; -... IEA.

Rh May P. 1455137; Prod. Calcium dependent cytosolic phospholipase A. .; IEA.

Roj GO:0004652; Frealcium-dependent cytosolic phospholipase A. .; IEA.

Roj GO:0004652; Frealcium-independent Cytosolic phospholipase A. activity; IEA.

Roj GO:0004652; Freareted phospholipase A. activity; IEA.

Roj GO:0004664; Freecreted phospholipase A. activity; IEA.

Roj GO:000468; Phospholipase A. activity; IEA.

Roj Roj GO:000468; Phospholipase A. activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 CCAAHDCCYDRLEDLGCGTKSLDYNFKYSRGEITCSVNQDFCGQQLCHCDRLLAECLAQH 123
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                                                                                                                      TDWCCCYTHDCCYNRLERKRGCGTKFLIYKFSYRGGRISCSTNQDSCRKQLCQCDKAAABCF 120
                                                                                           TDWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCL 119
                    MELALLCGLVVWA-GVIPIQGGILNLNKWVKQVTGKMPILSYWPYGCHCGLGGRGQPKDA 59
                                              4 LELLAALIMVFGPIQIQGSLAELNRMIWQLIGMRAGLSYAFYGCHCGLGGRGSPKDATDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
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SRC-ASSOCIATED PHOSPHOLIPASE A2.
: F5E0A76CE441772C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53; Indels
                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 25, Last annotation update)
Stc-associated phospholipase A2 precursor (EC 3.1.1.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.7%; Score 389; DB 11; 48.3%; Pred. No. 6.7e-37;
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                                                                                                                                                                                                                                                                                                154 AA
                                                                                                                                                                    KRNLDTYQKRLRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                        121 ARNKKSYSLKYQFYPNKFCKGKTPSC 146
                                                                                                                                                                                                                                                                                                                                                                                                                        Mesocricetus auratus (Golden hamster)
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                                                                                                                                                                                                                                                                                                PRT;
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PROSITE; PS00119; PA2 ASP; 1.
PROSITE; PS00118; PA2 HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 48.3
nes 69; Conservative
                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10036;
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Arita M., Muasshino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Arita M., Muasshino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
A Denki T., Sato H., Ota T., Wakamatsu A., Ishili S., Yamamoto J.,
A Denki T., Sato H., Ota T., Wakamatsu B., Kimura K.,
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
A masshita H., Matsuo K., Nachori K., Sekine M., Kikuchi H., Kanda K.,
A Magatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B.,
A Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AKO9366; BACO4210.1;
C. Submitted (JUL-2002) F:calcium ion binding; IEA.
GO; GO:0004623; F:phospholipase A2 activity; IEA.
BG; GO:0016042; P:lipid catabolism; IEA.
BRIAT, RP00068; PhospholipaseA2.
BRIAT, PR00181; PhospholipaseA2.
BRIAT, PR00181; PhospholipaseA2.
BRIAT, PR00181; PhospholipaseA2.
BRIAT, PR00181; PhospholipaseA2.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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45.5%; Pred. No. 1.4e-32;
ive 19; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l protein.
168 AA; 18586 MW; 35B1592A34A6A762 CRC64;
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01-077-2002 (TrEMBLrel. 22, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                              Last annotation update)
                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 AA
Æ.
168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 N--QTYREEYRGFLNVYCQGPTPNC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                   Hypothetical protein FLJ36326.
Homo sapiens (Human).
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     PRELIMINARY;
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TISSUE=Brain;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Thymus;
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PRINTS; PR00389; PHPHLIPASEA2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DWCCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 MAGVIP-----IQGGIINLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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8
L Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005509; R:adlcium ion binding; IEA.

GO; GO:0006529; F:calcium ion binding; IEA.

R GO; GO:0016642; F:phospholipase A2 activity; IEA.

R GO; GO:0016042; P:lipid catabolism; IEA.

R InterPro; IPR001211; PhospholipaseA2.

R Ffam, PF00068; PHPHLIPASRA2.

R PRINTS; PR00389; PHPHLIPASRA2.

R PRINTS; PR000819; PHPHLIPASRA2.

R SMART; SM00085; PA2.

R PROSITE; PS00118; PA2—ASP; 1.

H YPOCHCHICAL PROCEIN.
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PRINTS; PR00389; PHPHLIPASEA2.
Proom, PD000303; PhospholipaseA2; 1.
SWART; SW0085; PA2c; 1.
PROSITE; PS00118; PA2 HIS; 1.
SEQUENCE 210 AA; 23259 MW; 5ACS5CD96F68FC29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 187 AA; 20811 MW; 2DAA2274359A3A60 CRC64;
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Last sequence update)
Last annotation update)
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MGD; MGI:1349660; Pla2g2e.
GG:0005509; F:calcium ion binding; IEA.
GG:0005639; F:calcium ion binding; IEA.
GG: G0:0004623; F:phospholipase A2 activity; IEA.
GG: G0:0016042; P:lipid catabolism; IEA.
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STRAIN=C27BL/6J, TISSUE-Head;
MEDLINE=22354683; Pubmed=12466851;
The FANTOM CORBOTTIUM:
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169 RNLRSYNPQYQYF 181
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01-MAR-2003 (TrEMBLrel. 2.
01-MAR-2003 (TrEMBLrel. 2.
01-0CT-2003 (TrEMBLrel. 2.
Phospholipase A2.
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3 LALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW 62

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49 IAVLAGSVVITA----HSSLINLKSMVEAITHRNSILSFVGYGGYGGLGGRGHPMDEVDW 104
                                                                                                     63 CCQTHDCCYDHLKTQGCGIYKDYYRYNFSQGN-IHCSD-KGSWCEQQLCACDKEVAFCLK 120
                                                                                                                                                           105 CCHAHDCCYEKLFEQGCRPYVDHYDHRIENGTMIVCTELNETECDKQTCECDKSLTLCLK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andriao-Escarso S.H., Soares A.M., Rodrigues V.M., Angulo Y., Diaz C., Lomonte B., Gutierrez J.M., Giglio J.R.; Wyctoxic phospholipases A(2) in bothrops snake venoms: effect of chemical modifications on the enzymatic and pharmacological properties of bothropstoxins from Bothrops jararacussu.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kashima S., Soares A.M., Roberto P.G., Astolfi-Filho S., Pereira J.O., Silva M.X., Giulliati S., Farias M. Jr., Giglio J.R., Franca S.C., "Analysis of Bothrops jararacussu Venomous Gland Transcriptome with Structural and Functional Categories: Gene Expression Profile of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 VLLVGV---EGSLFELGKMILOETGKNPAKSYGAYGCNCGVLGRGKPKDATDRCCYVHKC
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Lepidosauria; Squamata; Soleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN 2003 (TrEMBLrel. 24, Created)
01-JUN 2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myotoxic phospholipase A2-like (Myotoxic A2-like phospholipase)
Bothrops jararacussu (Jararacussu)
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EMBL, AY195200; AA027453.1; --
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0006623; F:lipid catabolism; IEA.
InterPro; IPR001211; Phospholipase A2 activity; IEA.
Filmid Catabolism; IEA.
Filmid Catabolism; IEA.
Filmid Catabolism; IEA.
Filmid Catabolism; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi M.A.F., Queiroz G.P., Radis-Baptista G., Yamane T.,
Camargo A.C.M.;
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46.3%; Pred. No. 1.4e-30;
tive 19; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 AA
                                                                                                                                                                                                                                              121 RNLDTYOKRLRFYWRPHCRGOTPGC 145
                                                                                                                                                                                                                                                                                             165 DH--PYRNKYRGYFNVYCQGPTPNC 187
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MEDLINE=20472069; PubMed=11018293;
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Q7T3S7
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The FANTOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

The All of Genome Exploration Research Group Phase I & II Team;

The All of Genome Exploration Phase I & II Team;

The Theorem Consortium of the mouse transcriptome based on functional annotation of Genome Consology in the mouse transcriptome based on functional annotation of Genome Consology is realcium ion binding; IEA.

The Mature 420: 573 (2002).

The Mature 420: 573 (2002).

The Mature 420: 573 (2002).

The Mature 420: 573 (2003).

The Mature 420: 573 (2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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Trimeresurus flavoviridis (Habu).
Trimeresurus flavoviridis (Habu).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 38.7%; Score 330; DB 11; Length 2 il Similarity 44.3%; Pred. No. 6.1e-30; 58; Conservative 24; Mismatches 43; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                          (TremBirel. 23, Last sequence update) (TremBirel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                        Calcium-dependent phospholipase A2 precursor.
                                                                                                                                                                                                   202 AA.
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                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23,
                                                                            123 ҮКҮНЬКРЕСККАБР 136
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                                                                                                                                                                                                      PRELIMINARY;
                              LRFYWRPHCRGQTP
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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SEQUENCE FROM N.A.
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01-OCT-2003
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                                                                                                                                                                                                      Q8BJ93
                                                                                                                                                        RESULT 7
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70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 CYE--KLIDCSPKSDIXSYSWKIGVIICGE-GTECEKQICECDRAAAVCFGQNLRTYKKK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 IVAVWLIAVEGNLYQFGRMIWNRTGKLPILSYGSYGCYCGWGGQGPPKDATDRCCLVHDC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jasti J., Murugan P., Alagiri S., Singh T.P.; "X-ray structure of acidic phospholipase A2 from Indian saw-scaled-viper (Echis carinatus) with a potent platelet aggregation inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 VVMAGVIPIQGGILNILNIQVVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC
Chijiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M., Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.; "Interisland mutation of a novel phospholipase A2 from Trimeresurus flavoviridis venom and evolution of crotalinae group II phospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Echis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.9%; Score 314; DB 13; Length 138; 44.9%; Pred. No. 2.8e-28; tive 19; Mismatches 50; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY268946; AAP41217.1; -.
Hydrolase.
                                                                                                                                                  the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                          Prodom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
PROSITE; PS00119; PA2_ASP; 1.
PROSITE; PS001118; PA2_BS; 1.
SEQUENCE 138 AA; 15817 MW; A2F7B5A23897ECC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-007-2003 (TrEMBLrel. 25, Created)
01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Phospholipase A2 (EC 3.1.1.4).
Echis carinatus (Saw-scaled viper)
                                                                                                                                                  Submitted (FEB-2003) to the EMBL/GenBank/DDBJ dat
EMBL, AB102728; BAC56892.1; -
GO, GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004623; F:phospholipase A2 activity; IEA.
GO; GO:00160422; P:lippid catabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 AA
                                                                                                                                                                                                                                                                                            InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 LRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 YMPYPDFLCTDPTEKC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Venom gland;
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Best Local Similarity
Matches 56; Conserv
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Best Local Similarity
Matches 61; Conserv
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69 65

Gaps

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RESULT 10 Q805A2

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66 CYG--RANGCDPKLSTYSYNFQNGNIVCGNKYG-CLRHICECDRVAAICFQKNMYTYNKK 122
                                                                                                                                                                                                                                                                                                                                                                             70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
      MEDLINE=22707820; PubMed=12823540;
Guillemin I., Bouchier C., Garrigues T., Wisner A., Choumet V.;
"Sequences and structural organization of phospholipses A2 genes from
"Yipera aspis aspis, V. aspis zinnikeri and Vipera berus venom.
Identification of the origin of a new viper population based on
ammodytin II heterogeneity.";
Eur. J. Biochem. 270:2697-2706(2003).
EMBL; AY158636; AAN59982.1; ..
SEQUENCE 138 AA; 15716 MW; 7989F9E0D16C9CCB CRC64;
                                                                                                                                                                                                                                                                                               10 VVMAGVIPIQGGILNLNKNVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC
                                                                                                                                                                                                                                                                                                                      87 RYNFSQGNIHCS---DKGSWCEQQLCACDKEVAFCLKRNLDTYQKRLR--FYWRPHC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 OFTIVNGTVICGCTVASSCLCGQKACECDKQSVYCFKENLATYEKAFKQLFPTRPQC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 KMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGIYKDYY
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                    DB 13; Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 150;
                                                                                                                                                                                                                                                             55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC029347; AAH29347.1;
GO; GO:0005623; F:calcium ion binding; IEA.
GO; GO:0004623; F:phospholipase A2 activity; IEA.
GO; GO:0016042; F:lipid catabolism; IEA.
InterPro; IPR001211; PhospholipaseA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2c; 1.
PROSITE; PS00118; PA2_ASP; 1.
PROSITE; PS00118; PA2_ASP; 1.
SEQUENCE 150 AA; 16985 MW; 6548C632B1C2ECEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 34.8%; Score 296.5; DB 11; Similarity 45.3%; Pred. No. 3.3e-26; 53; Conservative 14; Mismatches 45;
                                                                                                                                                                                                                  36.0%; Score 306.5; DB 1
37.5%; Pred. No. 2.1e-27;
tive 27; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similar to phospholipase A2, group IIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | : | : | 123 YKNYSSSNCQENSDKC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 LRFYWRPHCRGQTPGC
                                                                                                                                                                                                                                                        51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                     Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Kidney;
                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYMPYGCHCGLGGRGQPKDATDWCCQTHDC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Chijava T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M.,
Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.;
Interisland mutation of a novel phospholipase A2 from Trimeresurus
flavoviridis venom and evolution of crotalinae group II phospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vipera berus berus (Common viper).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Viperinae, Vipera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.3%; Score 309; DB 13; Length 138; 44.1%; Pred. No. 1.1e-27; ive 19; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A2."; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AB102729; BAC56893.1; -0. GO:0005609; Exalcium ion binding; IEA. GO; GO:0004623; F:phospholipase A2 activity; IEA. GO; GO:0016042; F:lipid catabolism; IEA. InterPro; IPR00111; PhospholipaseA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00119; PA2 ASP; 1.
PROSITE; PS00118; PA2 HIS; 1.
SEQUENCE 138 AA; 15803 MW; A2F103123897ECC5 CRC64;
                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                              138 AA.
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SMART; SM00085; PA2c; 1.
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                    Trimeresurus flavoviridis (Habu)
130 LRFYWRPHCRGQTPGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 LRFYWRPHCRGQTPGC 145
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                                        123 YKSÝ--EDČTEEVQEĆ
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                                                                                                                                          PRELIMINARY;
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Best Loca Matches

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RESULT 11

Q7T1D5

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70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
                                                                                                                                                                                                                                                                                                                                                                                                 66 CYG--KVTGCDPKIDSYTYSKKNGDVVCGGDDP-CKKQICECDRVATTCFRDNKDTYDIK 122
                         "Functional and structural Analysis of Acidic and Basic Phospholipases A2 from Bothrops jararacussu Snake Venom."; Submitted (Aug-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX145836; AAN37410.1;
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004623; F:phospholipase A2 activity; IEA.
InterPro; IPR001211; PhospholipaseA2.
                                                                                                                                                                                                                                                                                                                                         10 VVMAGVIPIQGGILNLNKAVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC
Roberto P.G., Kashima S., Soares A.M., Astolfi-Filho S., Giglio J.R.,
                                                                                                                                                                                                                                                                                             54; Indels
                                                                                                                                                                                                                                      513647907BFD0F4E CRC64;
                                                                                                                                                                                                                                                                34.5%; Score 294; DB 13;
39.7%; Pred. No. 5.8e-26;
tive 22; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ammodytin II heterogeneity.";
Eur. J. Biochem. 270:2697-2706(2003).
EMBL, AX243575; AA086503.1; -
SEQUENCE. 138 AA; 15550 MW; 28C7496
                                                                                                                                                Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHLIPASEA2.
ProDom; PD000303; PhospholipaseA2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vipera aspis aspis (Aspic viper)
                                                                                                                                                                                          SMART; SM00085; PA2c; 1.
PROSITE; PS00119; PA2 ASP; 1.
SEQUENCE 138 AA; 15456 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 LRFYWRPHCRGQTPGC 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.0%;
39.0%;
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Matches 54; Conservative
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nes 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Matches
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TISSUBE-verom gland;
MEDLINE=22157211; PubMed=12167491;
Andriao-Escarso S.H., Soares A.M., Fontes M.R., Fuly A.L.,
Correa F.M., Rosa J.C., Greene L.J., Giglio D.R.,
"Structural and functional characterization of an acidic platelet
aggregation inhibitor and hypotensive phospholipase A(2) from Bothrops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 VVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                               Yong-Hong J., Yang J., Run-Qiang C., Dong-Sheng L., Xing-Ding Z., Wan-Yu W., Yu-Liang X., "A novel phospholipase A2 from Vipera russelli siamensis: isolation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Curracto, Jataicos, Contrata Craniata; Vertebrata; Euteleostomi;
Ediaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Viperinae, Vipera.
VOCH_TaxID=228341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                              34.7%; Score 295.5; DB 13; Length 39.0%; Pred. No. 3.9e-26; tive 23; Mismatches 57; Indels
                                                                                                                                                                                                                              cloning and sequence comparison.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000303; PhospholipaseA2; 1.
SWART; SW000B5; PA2c; 1.
PROSITE; PS00118; PA2 ASP; 1.
SEQUENCE 138 AA; 15401 MW; EB86AB6D46430DF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Tremblrel. 23, Created)
(Tremblrel. 23, Last sequence update)
(Tremblrel. 25, Last annotation update)
                                     01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                       EMBL; AY256974; AAP13805.1;
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004623; F:phospholipase A2 activity; IEA.
GO; GO:0016042; P:lipid catabolism; IEA.
InterPro; IPR001211; PhospholipaseA2.
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHIIPASEA2.
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Biochem. Pharmacol. 64:723-732(2002)
                        Created)
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                                                                  Phospholipase A2-I.
Vipera russelli siamensis.
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                        (TrEMBLrel.
                                    (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bothrops jararacussu
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SEQUENCE FROM N.A.
TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viperidae, Crotal
NCBI_TaxID=8726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003
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                        01-JUN-2003
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Matches
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Length 138;

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70 CYDHLKTQGCGIYKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLDTYQKR 129
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                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE=22707820; PubMed=12823540; MEDINE=22707820; PubMed=12823540; MEDINE=22707820; Bouchier C., Garrigues T., Wisner A., Choumet V.; Guillemin I., Bouchier C., Garrigues T., Wisner A., Ground structural organization of phospholipase A2 genes from Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom. Identification of the origin of a new viper population based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 VVMAGVIPIQGGILNINKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDWCCQTHDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                    Eukaryota; Metažoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Vipera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 289.5; DB 13; Length; Pred. No. 1.9e-25; 21; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36503.1; -. 15550 MW; 28C749C004DE408E CRC64;
(TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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qq

Search completed: October 5, 2004, 19:24:02 Job time : 30.8067 secs

age Blank (uspto)

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

October Run on:

5, 2004, 18:50:04 ; Search time 138.747 Seconds (without alignments) 1232.039 Million cell updates/sec

US-09-830-321A-2 Title: Perfect score:

3235 1 MIEVELSPTLALCLERVASH.......EQLLEALRQAVQRRRQRRPH 605 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

1586107

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:* A_Geneseq_29Jan04: geneseqp1980s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	1	Trimon	i miliari	Human	CPLAZ	Human	Adystos/ Human PLA	ruosbu	Human		Nove	Novel	Aaw75132 Human sec	7 Human	Abo01943 Novel hum	S Nove	Human	4 Human	T Himan	4	North	1000	Amino	4 Human	Novel	Mouse	Abb09147 Mouse pho
SUMMARIES	£		AAB03628	AAU10696	ABG76482	AAII1 0 6 9 7	ABG76483	AAY51557	AAB74635	AARA2415	AAR21140	ARG05871	7.0000mg	ADGZ U LOA	AAW / 51.32	AAW/5067	ABC01943	AB002008	AAE22843	ADB61634	ABB07497	ADC10174	ABG05869	ABB78290	ABB09144	ADE08121	ABR09149	ABB09147	45000t4
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ALIGNMENTS

Human; phospholipase 2; HPPL2; cancer; autoimmune disorder; inflammatory disorder; reproductive disorder; infection. [abel= potential_phosphorylation_site label= potential_phosphorylation_site label= potential_phosphorylation_site label= potential_phosphorylation_site label = potential_phosphorylation_site label= potential_glycosylation_site label= potential_glycosylation_site Location/Qualifiers AAB03628 standard; protein; 605 AA. Human phospholipase 2 HPPL2. 05-OCT-2000 (first entry) Key Modified-site Homo sapiens AAB03628; RESULT 1 AAB03628

552 /label= potential_phosphorylation_site

Modified-site

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The present sequence is human phospholipase 2 (HPPL2). This protein is involved in the hydrolysis of membrane phospholipids. The protein and its coding sequence can be used to diagnose and treat the following: cancers such as prostate, breast and testicular cancers, autoimmune and inflammatory disorders such as ALDS, allergies, anaemia, asthma, atherosclerosis, Cronn's disease, diabetes mellitus, emphysema, Graves', disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, psoriasis, rheumatoid arthritis and systemic lupus erythematosus, infection caused by viruses, fungi, bacteria, parasites and protozoa, and reproductive disorders including infertility, disruptions of the menstrual cycle, polycystic ovary syndrome, ectopic pregnancies, disruptions of spermatogenesis, cancers within the reproductive tract and
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                                                                                                                                                                                                                                                                                 Human phospholipase genes and proteins useful to diagnose, prevent treat cancer, autoimmune or inflammatory or reproductive disorders.
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         /label= potential_phosphorylation_site
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Pred. No. 4.3e-292;
0; Mismatches 0;
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N-PSDB; AAA53270.
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les 605; Conserv
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                        Calcium-independent cytosolic phospholipase A2-beta; cPLA2-beta; U937 cell; membrane phospholipid turnover; intracellular signalling; arachidonic acid cascade; inflammatory disorder; rheumatoid arthritis; psoriasis; asthma; inflammatory bowel disease; antiinflammatory.
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541 PEBAAGEVNISSSDSPYHYTKYTYSQEDVDKLLHITHYNVCNNQEQLLEALRQAVQRRR
                                                       GAFQQLQLLGRFCQEQGIPFPPISPSEGOLQPRECHTFSDPTCPGAPAVLHFSSGVRRT
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87.6%; Pred. No. 2.5e-248;
iive 5; Mismatches 22;
                                                                                                                                                                                                                                                                   AAU10696 standard; protein; 778 AA.
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N-PSDB; AAS17362.
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antiinflammatory; arachidonic acid cascade; enzyme;
inflammatory condition.
                                                           LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG
                                                                                                                   NOANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH
                                                                                                                                                                           226 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGFCAEEQAFLSRRKQVVAAALRQALQLDGD
                                                  LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP
                                                                               EWSOKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA
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                       ---LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD
                                                                                                                                                                                               FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF
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99US-00460145.
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13-DEC-1999;
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The invention relates to a purified phospholipase enzyme (calcium-independent cytosolic phospholipase A_2-beta enzyme) peptide appearing as ABG76482 encoded by a polynuclectide appearing as ABK118883. The protein has an enzymatic activity in a mixed micelle assay (MMA) with 1-palmitoyl -2- (^1.4C)-arachidonyl- phosphatidylcholine. cpLA2-beta is useful for assaying chemical agents for antiinflammancory activity mediated by the various components of the arachidonic acid cascade. cpLA2-beta is also various components of the arachidonic acid cascade. cpLA2-beta is also are useful in the development of polyclonal and monoclonal antibodies which are useful as research or diagnostic tools, and to study phospholipase A_2 activity and inflammatory conditions. The present sequence represents a partial cPLA2-beta protein
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Novel purified calcium-independent cytosolic phospholipase A2-beta enzyme, useful for screening compounds having antiinflammatory activity mediated by the arachidonic acid cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 TGLLVLFCPAPCFFFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTFRFHCPA-C----WEQE-LSI------RLQDAPBEQLKAPLSALPSGQVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IRELAVRIGEGPCAEEQAFLSRRKQVVAAALRQALQLDGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2767.5; DB 6;
Pred. No. 2.5e-248;
; Mismatches 22;
                                                                                                     Claim 2; Col 13-18; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.5%;
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Matches 537; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 778 AA;
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us-09-830-321a-2.rag

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The invention relates to a purified phospholipase enzyme (calciumindependent cycosolic phospholipase A.2-beta enzyme) peptide appearing as ABG76482 encoded by a polymucleotide appearing as ABX118883. The protein has an enzymatic activity in a mixed micelle assay (MMA) with 1-palmitoyl-2-(1/4C)-arachidonyl-phosphatidylcholine. CPLA2-beta is useful for assaying chemical agents for antiinflammatory activity mediated by the various components of the arachidonic acid cascade. CPLA2-beta is also useful in the development of polyclonal and monoclonal antibodies which
                                                                                                                                                                        SAPGYRITPEEAAAGEVNLSSSDSPYHYTKYTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel purified calcium-independent cytosolic phospholipase A2-beta enzyme, useful for screening compounds having antiinflammatory activity mediated by the arachidonic acid cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; calcium independent cytosolic phospholipase A2-beta; cPLA2-beta; antiinflammatory; arachidonic acid cascade; enzyme; inflammatory condition.
                                                                                                                                                                                                                                    QOLQLIGRFCQBQGIPFFPISPSPEBQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY
425 ILHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG
                                                                                         NQANLDKBQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH
                                                                                                           FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF
                                                                                                                                                                                                                                                                      -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL
                             AFI PSELFCSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR
                                              484 QQLQLLGRECQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cytosolic phospholipase A2-beta, cPLA2-beta.
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N-PSDB; ABX11884.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a novel calcium-independent cytosolic phospholipase A2 (cPLA2)-beta enzyme and the cDNA sequence encoding it. The cDNA clone is isolated from U937 cells. The cPLA2 enzyme is active in membrane phospholipid turnover and in regulation of intracellular signalling mediated by the arachidonic acid cascade. The invention describes a method for producing phospholipase enzymes which can be used to identify inhibitors of their function. The inhibitors can used to treat inflammatory disorders such as rheumatoid arrhritis, psoriasis, asthma, and inflammatory bowel disease. The present sequence represents cPLA2 N-terminal peptide-cPLA2-beta fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calcium-independent cytosolic phospholipase A2-beta; cPLA2-beta; mutant; U937 cell; membrane phospholipid turnover; intracellular signalling; arachidonic acid cascade; inflammatory disorder; rheumatoid arthritis; psoriasis; asthma; inflammatory bowel disease; antiinflammatory; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytosolic phospholipase A2-beta enzyme encoding polynucleotide.
. for producing the enzyme for use in assays to discover enzyme
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                                                                                                                     cPLA2 N-terminal peptide-cPLA2-beta fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.5%; Score 2767.5; DB 5
87.6%; Pred. No. 2.6e-248;
cive 5; Mismatches 22;
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                             AAU10697 standard; protein; 797
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                                                                                          (first entry)
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N-PSDB; AAS17363.
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                                                                                                                                                                                                                                           Synthetic.
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An isolated amino acid having phospholipase (PL)A2 activity is useful in assays to identify inhibitors having a therapeutic benefit, such as inhibiting the central role of PLA2 in the inflammatory component of

Claim 1; Col 53-58; 32pp; English.

Alzheimer's disease.

RT;

Pickard

RM,

Kramer

Choiu XC,

(ELIL) LILLY

WPI; 2000-181816/16. N-PSDB; AAZ88756, AAZ88757 Sharp JD, Strifler BA,

97US-00827208 96US-0014608P

28-MAR-1997; 29-MAR-1996;

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are useful as research or diagnostic tools, and to study phospholipase A 2 activity and inflammatory conditions. The present sequence represents the cPLA2-beta protein
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                                                                                         TGLLVLFCPAPCPFFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR
                                                                                                         203 TGTFRFHCPA-C----WEQE-LSI------RLQDAPBEQLKAPLSALPSGQVVR
                                                                                                                               --LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD
                                                                                                                                             245 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGFCAEEQAFLSRRKQVVAAALRQALQLDGD
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                                                                             Gaps
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                                                        DB 6;
                                                       85.5%; Score 2767.5; DB 6, 87.6%; Pred. No. 2.6e-248; ive 5; Mismatches 22;
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                                                              Best Local Similarity 87.8
Matches 537; Conservative
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This invention describes a novel human phospholipase A2 (PLA2) protein (I) and its encoding nucleic acid. The amino acid (I) releases archidonic acid in specific tissues characterized by unique membrane phospholipids, by generating 19sophospholipid species which are deleterious to membrane integrity or by remodeling of unsaturated species of membrane phospholipids through deacylation/reacylation mechanisms. The therapeutic benefit, such as inhibiting the central role of PLA2 in the inflammatory component of Alzheimer's disease. The amino acid (I) allows sensitive and rapid screening and identification of inhibitors of phospholipase A2. This sequence represents the human PLA2 protein (also known as phosphatide 2-acyl hydrolase)
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                                                                                                                                                                                                                                                                                                                                   LOEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP
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PLA2; phospholipase A2; phosphatide 2-acyl hydrolase; human; therapy; arachidonic acid; lysophospholipid; Alzheimer's disease.

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913

AAY51557 standard; protein;

AAY51557 RESULT

(first entry)

18-MAY-2000

AAY51557

Human PLA2 protein

Homo sapiens JS6025178-A. S FEB 2000

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07-FEB-2000;
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Comprising a 3085 base pair phospholipase A2 (PLA2) sequence (given in AAF74999), encoding a 913 residue phospholipase A2 protein sequence

Cg (given in AAB74635), or a nucleotide sequence which hybridises under (given in AAB74635), or a nucleotide sequence which hybridises under stringent conditions to the above mentioned mucleotide sequence. Also described are: (1) an isolated polynucleotide (II) comprising an 8517 comprising (I) and an expression control sequence; (3) a host cell transformed with (III); (4) an expression vector (IV) comprising (II) comprising (II) and an expression control sequence; and (5) a host cell cransformed with (IV). (I) is useful for screening compounds which cransformed or transformed or transform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid molecules encoding phospholipase A2 enzyme, useful in screening assays for identifying compounds that inhibit or block phospholipase A2 enzyme activity.
                 592
                                    SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 900
                 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL
                                                                                                                                                                                                                                                                                                                                                                Phospholipase A2; PLA2; antiinflammatory; inflammatory condition; rheumatoid arthritis; psoriasis; asthma; cytosolic PLA2; cPLA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2767.5; DB 4; Length 913; Pred. No. 3.2e-248; 5; Mismatches 22; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sharp JD, Strifler BA;
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                                                                                                                                                                                                                           AAB74635 standard; protein; 913 AA.
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97US-00827208.
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                                                                                               RQAVQRRRQRRPH
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9

Gaps

49;

vuery Match 85.5%; Best Local Similarity 87.6%; Matches 537; Conservative

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                                                                                                                                                                               AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
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                                                                                                                                                                                                                                                                                                                     SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNOEQLLEAL
                                                                                                                                                                                                                                                                                                      PSTWKATILDGLPNOLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF
                                                                                                                                                                                                                                                                                                                                                                                                 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL
                                                                                     LIHDEPHDHKLSDOREALSHGONPLPIYCALNTKGOSLTTFEFGEWCEFSPYEVGFPKYG
                                           LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP
                                                                                                                   EWSOKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA
                          ----DRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD
-----RLODAPEEOLKAPLSALPSGOVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phospholipase A2; PLA2; bPLA2, PLA2-beta; inhibitor; screening; antiinflammatory; human; Alzheimer's disease; therapy.
                                                                                                                                                                                                                                                                                                                                                    QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF
      319 TGTFRFHCPA-C----WEOE-LSI----
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97US-0041264P.
97US-00827208.
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19-MAR-1997;
28-MAR-1997;
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BA
     Strifler
    Sharp JD,
  Pickard RT,
                          N-PSDB; AAF90487, AAF90488
  R.W.
                   2001-366537/38
Choiu XC,
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RESULT 9

Assays to evaluate the effectiveness of inhibitors of phospholipase A2, used to screen candidate compounds, comprise recombinant expression of novel phospholipase A2.

Claim 1(a); Col 53-58; 32pp; English.

The present sequence is that of a novel human phospholipase A2 (PLA2, also referred to bPLA2 or PLA2-beta). PLA2 liberates arachidonic acid from phospholipids, leading to the production of eicosanoids involved in inflammatory reaction. A claimed assay for evaluating the effectiveness transformed with an expression vector comprising PLA2 genomic DNA ocompound, and determining the PLA2, contacting it with a candidate compound, and determining whether the PLA2 activity has been inhibited. The assay provides rapid and efficient screening for new antinflammatory drugs that inhibit the arachidonic acid cascade. These may be especially useful in the treatment of the inflammatory component of Alzheimer's NAME OF COLORS OF STATES O

Sequence 913 AA;

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                                                                                                                                                                                                       LLHDEPHDHKLSDOREALSHGONPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
                                                                                                                                                                                                                                   600
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                                         --LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD
                                                                                                                        LOEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP
                                                                                                                                                                EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA
                                                                                                                                                                              LIHOEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFFFGEWCEFSPYEVGFPKYG
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                           49;
   85.5%; Score 2767.5; DB 4; Length 913; larity 87.6%; Pred. No. 3.2e-248; Conservative 5; Mismatches 22: Indels 49.
                          22; Indels
                      5; Mismatches
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           Similarity
                    537;
Query Match
Best Local S:
Matches 537,
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384 TAGRIABFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSE

LPESRICFLEGIWSNLYAANLODSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPS

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901

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New crystalline cytosolic phospholipase A2 (cPLA2) for identifying a species which is an agonist or antagonist of cPLA2 activity or binding that can be used to prevent or treat inflammation or inflammatory-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the human cytosolic phospholipase A2 (CPLA2) beta protein. The invention concerns the elucidation of the crystal structure of the protein and its use in drug design. The protein can be used to identify treatments for inflammation-related conditions such as rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease, and diseases such as osteoporosis, colitis, myelogenous leukaemia, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
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                                                                                                                           phospholipase A2 beta; CPLA2 beta; asthma; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 LRELAVRIGEGPCAEEQAFLSRRKQVVAAALRQALQLDGDLGEDETPVVAIMATGGGIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 MISLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 MISLYGOLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSCKDLAGPTELLKTQVTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2765.5; DB 3; Length 533;
Pred. No. 2.1e-248;
1; Mismatches 1; Indels 11;
                                                                                              Human cytosolic phospholipase A2 cPLA2 beta.
                                                                                                                                                                                                                                                                                                                                            Seehra JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                          Human; cytosolic phospholipase A2 beta;
inflammatory disease; crystal structure
                 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4; 71pp; English.
             AAB21140 standard; protein; 533
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                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 533 AA;
                                                                                                                                                                                               WO200047763-A1
                                                                                                                                                                                                                                                                                 15-FEB-1999;
                                                                                                                                                                    Homo sapiens
                                                                     19-JAN-2001
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AAB21140
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22238
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                                                                                                                                480
                                                                                                      552
503
                                                                                                                           SPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREYSAPGVRRTPEBAAAGEVNLS
                                                                                                   SPSPEEQLQPRECHTFSDPTCPGAPAVLHF-----SSGVRRTPEEAAAGEVNLS
                                                             PHLCLLDVGYLINTSCLPLLQPTRDVDL1LSLDYNLHGAFQQLQLLGRFCQEQGIPFPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                            SSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRRPH 605
                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 36230; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #5862.
                                                                                                                                                                                                                                                                     ABG05871 standard; protein; 1020 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-00540217.
2000US-00649167.
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                                                                                                                                                                                                                                                                                                                               (first entry)
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N-PSDB; AAS70058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2.
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23-AUG-2000;
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421
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                                                                                                                                                                                                                                                LIHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG
                                                                                                                                                                                                                             LQEDBIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP
                                                                                                                                                                                                                                                                                    184 EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA
                                                                                                                   24 TGLLVLFCPAPCPFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR
                                                                                                                                    -- LRELIAVRIGEGPCAEEQAFISRRKQVVAAALRQALQLDGD
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                                                                                          52;
                                                                  Length 1020;
                                                                                            Indels
                                                                83.5%; Score 2700; DB 4;
86.4%; Pred. No. 7.5e-242;
                                                                                             5; Mismatches
electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                                                   al Similarity 86.4
532; Conservative
                                            Sequence 1020 AA;
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97US-0043670P
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28-JAN-1999
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                                                                                                                                                                                                                                                polynucleotide (I) and polypeptide (II)
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                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.7%; Score 2610.5; DB 4; Length 1040; 84.3%; Pred. No. 1.7e-233;
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                                                                                                                                                                                                                  Claim 20; SEQ ID NO 50513; 103pp; English.
                                                                                                                                                                                                                                             The invention relates to isolated
  30-MAR-2001; 2001WO-US008631
                          31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                           Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 84.3
Matches 520; Conservative
                                                                                                               WPI; 2001-639362/73.
N-PSDB; AAS84341.
                                                                                           Liu C,
                                                                (HYSE-) HYSEQ INC.
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FREYSAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKL.HITHTHTHTHTH 1011
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772 RNQANLDKEQVPILKIEBPPSTAGRIAEFFTDLLTWRPLAQATQNFLRGRSIFHKDYFQH 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Albreimer; sdisease; restenosis; AlDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                              832 PHESTWRATTLDGLPNQLTPSEPHLCLLDGGYTLINTSCLPLQPTRDVDLILSLDYNLH
                                                                                                                                                   481 GAFQQLQLLGRFCQEQGIPFPPISPSEEQLQP-RECHTFSDPTCPGAPAVLHF-----
                                                                                                                                                                                                    892 GAFQQLQLLGRFCQEQGIPFPPISPSPERQLQPWRSCHTFSDPTCPGAPAVLHFPLVSDS
                                                   PHFSTWKATTLDGLPNQLTPSEPHLCLLDVGY-LINTSCLPLLQPTRDVDLILSLDYNLH
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HUMA-) HUMAN GENOME SCI INC.

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X Huben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;

Bednarik DP, Endress GA, Yu G, Ni J, Peng P, Young PB, Greene JM;

PI Bednarik DP, Endress GA, Yu G, Ni J, Peng P, Young PB, Greene JM;

PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;

PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;

N-PSDB; AAV34229.

XX

New isolated human genes and the secreted polypeptides they encode
Province detailed human genes and treatment of e.g. cancers, neurological

Bright of diagnosis and treatment of e.g. cancers, neurological

Bright of diagnosis and treatment of e.g. cancers, neurological

RX

NX

Claim 1; Page 326-327; 447pp; English.

XX

Claim 1; Page 326-327; 447pp; English.

XX

This sequence represents a secreted human protein encoded by the gene

CC clone detailed in the descriptor line. The gene can be used to generate

CC clone detailed in the descriptor line. The gene can be used to generate

CC clone detailed in the descriptor line. The gene can be used to generate

CC clone detailed in the descriptor line. The gene can be used to generate

CC clone detailed in the descriptor line. The proventing, treating

CC as compared to the human protein only. The invention relates to 70 novel

CC and locations which the are useful for preventing, treating

CC and sequences AAW3505-W75179) which are useful for preventing, treating

CC and location which closes are described for each of the

CC new polypeptides in a sample or by determining the amount of the

pathological conditions e.g. by protein or gene thrzapy.

CC new polypeptides in a sample or by determining the movel to correct

CC new polypeptides in a sample or by determining the movel to correct

CC new polypeptides in a secreted which tissues they are most highly expressed

CC new polypeptides in a secreted which is such as a secreted on which tissues they are most highly expressed

CC new polypeptides of the described uses). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-20

Sequence 483 AA;

Query Match 77.6%; Score 2509.5; DB 2; Length 483;

Best Local Similarity 96.9%; Pred. No. 1.3e-224;

Matches 467; Conservative 2; Mismatches 2; Indels 11; Gaps

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; ALDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                     Human secreted protein encoded by gene 11 clone HCENJ40.
                                                                                                                                                                                                                  Location/Qualifiers
29
                  AAW75067 standard; protein; 483 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Gr
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R,
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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  97US-0047590P

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N-PSDB; AAV34164.
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Human; immunoglobulin G; IgG; fragment of crystallisation; Fc; immune system disorder; haematopoietic cell disorder; inimunologic deficiolency disorder; ataxia telangiectasia; HIV infection; Miskott-Aldrich disorder; thrombocytopenia; haemoglobinuia; haemoglobinuia; blood coagulation disorder; blood platelet disorder; autoimmune disorder;
           close detailed in the descriptor line. The gene can be used to generate clusion proteins by linking to the gene to a human immunoglobulin Rc portion (e.g. AAV34145) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 70 novel genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino acid sequences AAW75057-W75179) which are useful for preventing, treating acid sequences namedical conditions e.g. by protein or gene therappy. Also, or ameliorating medical conditions can be diagnosed by determining the amount of the pathological conditions can be diagnosed by determining the amount of the new polymerlectides. Specific uses are described for each of the 70 polymuclectides, based on which issues they are most highly expressed in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct Pf field.) (Updated on 25-MAR-2003 to correct
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sequence represents a secreted human protein encoded by the gene
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Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis; glomerulonephritis; Grave's disease; allergic reaction; graft-versus-host disease; hyperproliferative disorder; neoplasm; infectious disease; nervous system disease; spinal cord disorder; andead trauma; stroke; tissue regeneration; congenital defect; trauma; wound; burn; incision; ulcer; age disease; osteoporosis; periodontal disease; liver failure; catabolism; anabolism; metabolism; food additive; preservative; secreted protein.
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23-MAY-1997;
23-MAY-1997;
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23-MAY-1997;
                                                                                       Homo sapiens.
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23-MAY-1997
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970S-0048964P.
970S-0056630P.
970S-0056631P.
970S-0056631P.
970S-0056632P.
970S-0056662P.
970S-0056662P.
970S-005664P.
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970S-005681P
970S-005681P
970S-005684P
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970S-005688P
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                                          22-AUG-1997;
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RUBEN S M.
ROSEN C A.
FISCHER C L.
SOPPET D R.
CARTER K C.
BEDNARIK D R. HU J. FLORENCE K A. NI J. FENG P. YOUNG P. GREENE J M. FERRIE A M. OLSEN H S. EBNER R. BREWER L A. Ġ (FISC/) (SOPP/) (CART/) (BEDN/) (YOUN/) (GREE/) (FERR/) (FLOR/) (OLSE/) (EBNE/) (BREW/) (YUGG/) (NIJJ/) (FENG/) (RUBE/)

Brewer LA; Greene JM; Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC; Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, G; Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R,

2003-466138/44. WPI; 2003-466138/ N-PSDB; ACD08035. Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing or treating deficiencies or disorders of the immune system, autoimmune disorders, hyperproliferative disorders, and infectious diseases.

Claim 11; Page 177-178; 243pp; English.

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the invertion describes an isolated human secreted HoDAZSO polypeptide from the invertion describes an isolated human secreted HoDAZSO polypeptide from polypeptide fragment of any one of the 123 polypeptide sequences of the polypeptide defined in the specification and having biological activity, polypeptide domain or repitope of PS, secreted form of PS, full-length complete in the specification and having biological activity, protein of PS, or variant, allelic variant or species homologue of PS. (I) or a polymucleotide (II) encoding (I) is useful for preventing, or anciprating a medical condition in a mammalian subject. (I) is useful for diagnosing a pathological condition in a subject. (I) is useful for inferity to a pathological condition in a subject. (I) is useful for inferity of the binding partner and determining whether the binding deficiencies of haematopoletic cells, to treat immunologic deficiency disorders of haematopoletic cells, to treat immunologic deficiency disorders, thrombocytopemia or haemoglobinuria, blood platelet disorders, autoimmune disorders are deficiency disorders, brombocytopemia or haemoglobinuria, blood platelet disorders, autoimmune disorders, dermitis, glomerulonephritis, Grave's disease), allergic reactions, cells of the standarder, brome breast, disease, haemolytic anaemia, rhuman or stroke), to capated in the abdomen, bone, breast, disease, and prizated cells reading to the regeneration defected in the abdomen, bone breast, disease, had trained when the abdomen, bone breast, disease, had trained when the abdomen, bone breast, disease, had the pr
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                    invention describes an isolated human secreted HODAZ50 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 BLLKTQVTKNKLGVLAPSQLQRYRQELABRARLGYPSCFTNLWALINEALLHDEPHDHKL
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97US-0057761P.
98WO-US004482.
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ROSEN C A.
PISCHER C L.
STORPET R C L.
CARTER K C.
BEDNARIK D R.
WINDRESS G A.
YU G.
NI J.
FENG P.
YOUNG P. E.
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05-SEP-1997;
05-SEP-1997;
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23-MAY-1997;
23-MAY-1997;
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23-MAY-1997;
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(ROSE/)
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22-AUG-1
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    Human; immunoglobulin G; IgG; fragment of crystallisation; Fc; immune system disorder; haematopoietic cell disorder; immunologic deficiency disorder; ataxia telangiectasia; HIV infection; Miskotr-Aldrich disorder; hrombocytopenia; haemoglobinuria; blood coagulation disorder; hrombocytopenia; haemoglobinuria; Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis; glave's disease; allergic reaction; glomerulonophritis; Grave's disease; allergic reaction; organisms; graft-versus-host disease; hyporproliferative disorder; neoplasm; infectious disease; nervous system disease; spinal cord disorder; head trauma; stroke; tissue regeneration; congenital defect; trauma; wound; burn; incision; ulcer; age disease; osteoporosis; periodontal disease; liver failure; catabolism; anabolism; metabolism; food additive; preservative; secreted protein.
   ABO02008 standard; protein; 483 AA.
                                                                                                                                                                    Novel human secreted protein #76.
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9705-004033P.
9705-004033P.
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the amino acid sequence of a novel human secreted protein
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         HU J.
FLORENCE K A.
GREENE J M.
FERRIE A M.
DUAN R.
               OLSEN H S.
EBNER R.
BREWER L A.
SHI Y.
                                                  N-PSDB; ACD08100.
                                     Ferrie AM,
                               Ruben SM,
Bednarik D
               (OLSE/)
(EBNE/)
(BREW/)
(SHIY/)
         (HUJJ/)
(FLOR/)
      DUAN/)
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Immunologic deliciency disorders, ataxia telangieticasia, his illuction, wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood coagulation disorders, thrombocytopenia or haemoglobinuria, blood coagulation disorders, blood platelet disorders, autoimmune disorders (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis, graver disease), allergic reactions, gratt-versus-host disease, hyperproliferative disorders (e.g., neoplasms located in the abdomen, bone, breast, digestive system, liver, pancreas, bacterial, fungal or parasitic infection), central and peripheral nervous differentiate, proliferate and attract cells leading to the regeneration of tissues to repair. replace or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g., suseporosis, periodontal disease, liver failure) or surgery. (I) or (IV) et suseful to modulate mammalian characteristics, to modulate mammalian characteristics, to modulate mammalian storage of energy, to change a mammal's mental state or physical state, or as a food additive or preservative, such as to increase or decrease cy storage capabilities, fat content, lipid, protein, carbohydrate, vitanins, minerals, cofactors or other nutritional components. This is (1) comprising a sequence at least structure an invariant purpreparted from polypeptide fragment of any one of the 123 polypeptide sequences (FS) fully defined in the specification and having biological activity, polypeptide domain or epitope of FS, secreted form of PS, full-length protein of FS, or variant, allelic variant or species homologue of FS. (7) or a polymucleotide (11) encoding (1) is useful for preventing, treating, or ameliorating a medical condition in a mammalian subject. (1) or a polymucleotide (11) encoding (1) is useful for preventing, treating, or ameliorating a medical condition in a subject. (1) is useful for identifying a binding partner and determining whether the binding partner affects the activity of the polypeptide. (1) or (11) is useful for diagnosing or treating deficiencies or disorders of the immune whether halvish disorders at a telangistetala, HIV infection, whether halvish disorders at a telangistetala, HIV infection, Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing or treating deficiencies or disorders of the immune system, autoimmune disorders, hyperproliferative disorders, and infectious diseases. Greene JM; Brewer invention describes an isolated human secreted HODAZ50 polypeptide Carter KC;
P, Young PE, Gren HS, Ebner R, Fischer CL, Soppet DR, Carter B GA, Yu G, Ni J, Feng P, Yor Hu J, Florence KA, Olsen HS, Claim 11; Page 210; 243pp; English. , DR, buan R, WPI; 2003-466138/44

Sequence 483 AA;

11; Gaps 77.6%; Score 2509.5; DB 6; Length 483; llarity 96.9%; Pred. No. 1.3e-224; Conservative 2; Mismatches 2; Indels 11; Query Match Best Local Similarity Matches 467; Conserv

135 MATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPT 194

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195 BLLKTQVTKNKLGVLAPSQLQRYRQELABRARLGYPSCFTNLWALINEALLHDBBHDHKL 254

61 ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL 120 LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGARQQLQLLGRRPCQ 494 543 EQGIPFPPISPSEERQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREYSAPGVRRTPEE 420 315 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP 375 LLKIEBPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG SDOREALSHGONPLPIYCALNTKGOSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSE EQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF-----SSGVRRTPEE 544 AAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRR 5, 2004, 19:21:35 Search completed: October Job time: 144.747 secs PH 605 PH 482 435 495 361 604 g ò d ò 셤 à 원 à 셤 à qq ð

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

5, 2004, 19:10:14; Search time 37.9133 Seconds (without alignments) 823.819 Million cell updates/sec October Run on:

US-09-830-321A-2

Title: Perfect score:

3235 1 MIFVELSPTLALCLERVASH......EQLLEALRQAVQRRRQRRPH 605 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

389414 Total number of hits satisfying chosen parameters:

389414 seqs, 51625971 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued Patents AA:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Semience 2. Appli		4	4	, w	, ~	· ~	144	200		ì		'n	4	, 2	ì ~	4		4	Sequence 5606, Ap	10.	Segmence 11. April	Sequence 121 Appr	Segmence 4623 An	Segmente A aprili	Sequence 16. Appli	Sequence 16, Appl
SUMMARIES	ID	US-09-460-145-2	US-09-895-547-2	US-09-460-145-4	-09	US-08-827-208-3	-09-500-358-	-09-498-	-09-148-	US-09-148-545-209	US-08-046-508-2	US-09-045-185-2	US-08-890-615-2	US-09-246-290A-2	US-09-687-538B-4	US-09-437-687A-2	US-10-263-250-2	US-09-621-976-4397	-538B-	US-09-205-258-342	US-09-621-976-5606	US-09-295-186-10	US-09-295-186-11	PCT-US95-17111A-121	US-09-621-976-4623	-53BB-6	US-09-437-687A-16	-250-
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	Query Match Length	778	778	797	797	913	913	913	483	483	749	541	541	541	638	654	654	90	640	87	99	552	573	397	117	627	648	648
o t e	Query Match	85.5	85.5	85.5	85.5	85.5	85.5	85.5	77.6	77.6	19.1	15.4	15.2	15.2	6.4	6.4	6.4	6.3	6.2	6.2	6.1	0.9	6.0	6.0	5.8	5.8	5.8	5.8
	Score			2767.5				767.	2509.5	20	619	498.5	490.5	490.5	208	208	208	203.5	2007	200	198.5	195.5		193	189	188		186.5
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Semience 121. App	Sequence 121, App	Sequence 121, App	•	18.	Sequence 16, Appl	24	22	32	30	20.		28.	26.	5592	573	573	884,	
US-08-454-557C-121	US-08-340-426D-121	US-08-450-673C-121	US-09-621-976-4482	US-09-295-186-18	US-09-295-186-16	US-10-020-079-24	US-10-020-079-22	US-10-020-079-32	US-10-020-079-30	US-10-020-079-20	US-10-020-079-18	US-10-020-079-28	US-10-020-079-26	US-09-621-976-5592	US-09-636-215-573	US-09-685-166A-573	US-09-685-166A-884	
7	N	N	4	ᡊ	٣	4	4	4	4	4	4	4	4	4	4	4	4	
375	375	375	87	649	612	116	789	863	876	889	895	916	982	120	132	132	135	
5.7	5.7	5.7	5.6	5.5	5.5	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5.3	
185	185	185	182.5	177.5	177	176	176	176	176	176	176	176	176	171	171	171	171	
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Kriz, Ron
APPLICANT: Song, Chuanzheng
TITLE OF INVENTION:
CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: POLYDOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/460,145
FILLING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI5289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/788,975
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                  Sequence 2, Application US/09460145 Patent No. 6287838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G1526
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 498-8224
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 778 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-09-460-145-2
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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COUNTRY:
ZIP: 0214
US-09-460-145-2
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83 Gaps 46. Query Match
Best Local Similarity 87.6%; Pred. No. 2.1e-268;
Matches 537; Conservative 5; Mismatches 22; Indels 49;

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24 TGLLVLFCPAPCPFFFFFFFFFFSUSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR

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LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
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                                                                                                                                                                                                                                                                                                          24 TGLLVLFCPAPCPFFFFFEMESLSVAQAGVOWRDLGSLQPPPLGFKRFSCLSLPSSWDYR
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Patent No. 6287838
GENERAL INFORMATION:
APPLICANT: Kriz, Ron
APPLICANT: Kriz, Ron
APPLICANT: Cyrosolic Phospholipase A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                             22; Indels
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Local Similarity 87.6%; Pred. No. 2.1e-268;
nes 537; Conservative 5; Mismatrher
        REFERENCE/DOCKET NUMBER: GIS289
TELECOMMUNICATION INFORMATION:
TELEPHONE: (6.17) 498-8224
TELEFAX: (6.17) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
REGISTRATION NUMBER: 32,724
                                                                                                                LENGTH: 778 amino acids TYPE: amino acid
                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQAVQRRRQRRPH 605
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US-09-460-145-4
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                                                                                                                                                                                                                                                                                                   AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
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     ----RLQDAPEEQLKAPLSALPSGQVVR
                                                                   226 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Song, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PLOSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/460,145
APPLICATION NUMBER: 09/460,145
FILING DATE: «UNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
      184 IGTFRFHCPA-C----WEQE-LSI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09895547 Patent No. 6482625 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROAVORRRORRPH 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Cambridge
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kriz, Ron
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US-09-895-547-2
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      665 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 724
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                                              534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNOEOLLEAL
                                                                             SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL
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                                                                                                                                                                                                                                                                                                                                                           Song, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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Best Local Similarity 87.6%; Pred. No. 2.2e-268,
Matches 537; Conservative 5; Mismatches 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURPER I BM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURPENT APPLICATION DATA:
APPLICATION NUMBER: US/09/895,547
FILING DATE: 29-Unn-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: G15289 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/460,145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                              Sequence 4, Application US/09895547
Patent No. 6482625
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
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ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
                                                                                                                                593 RQAVQRRRQRRPH 605
                                                                                                                                                                   785 RQAVQRRRQRRPH 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 364
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                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CAURENY APPLICATION DATA:
APPLICATION NUMBER: US/09/460,145
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
               ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: MA COUNTRY: USA
                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15289
TELECOMMINICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/788,975
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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Matches 537; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                         02140
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124 LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 183
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APPLICANT: Kramer, Ruth M.
APPLICANT: Kramer, Ruth M.
APPLICANT: Sharp, John D.
APPLICANT: Starp, John D.
APPLICANT: Strifler, Beth A.
ITTLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 4
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                            DB 3;
                                                                                                                                                                      Score 2767.5; DB 3,
Pred. No. 2.7e-268;
5; Mismatches 22;
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Patent No. 6197569
GENERAL INFORMATION:
TELEPAX: (317) 276-3861

JINFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: DOLLGY: 11near
MOLECULE TYPE: Protein
US-08-827-208-3
                                                                                                                                                                            85.5%;
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537; Conserv
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US-09-500-358-3
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Best Local
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   LLHDEPHDHKLSDQREALSHGONPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
                                                                                     485 AFIPSELFGSEFFMGOLMKRLPESRICFLEGIWSNLYAANLODSLYWASEPSOFWDRWVR 544
                                                                                                                                                                                                                 NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 423
                                                                                                                                                                                                                                                                                             FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
                                                                                                                                                                                                                                                                                                                                                                                            725 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 784
                                                                                                                                                                                                                                                                                                                                                                                                                                               -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL
                                                                                                                                                                                                                                                                                                                                                                      QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chiou, Xue-Chiou C.
APPLICANT: Kramer, Ruth M.
APPLICANT: Share, Bichard T.
APPLICANT: Sharp, John D.
APPLICANT: Strifter, Bach A.
ITILE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/827,208

FILING DATE: 28-MAR.1997

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 60/014,608

FILING DATE: 29-MAR.1996

PRIOR APPLICATION NUMBER: US 60/014,608

FILING DATE: 29-MAR.1996

PRIOR APPLICATION NUMBER: US 60/041,264

FILING DATE: 19-MAR.1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana COWIRY: United States of America ZIP: 46285 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-827-208-3
; Sequence 3, Application US/08827208
; Patent No. 6025778
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQAVQRRRQRRPH 605
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CORRESPONDENCE ADDRESS:
                                                                                                    425
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841 SAPGVRRTPBEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LRELAVRIGEGPCAEEQAFLSRRKQVVAAALRQALQLDGD 123
                              781 QQLQLLGRFCQEQGIPFPPISPSPERQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREY 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 49; Gaps
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484 QQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Chiou, Xue-Chiou C.
APPLICANT: Kramer, Ruth M.
APPLICANT: Fichard, Richard T.
APPLICANT: Sharp, John D.
APPLICANT: Strifler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED TITLE OF INVENTION: MUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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87.6%; Pred. No. 2.7e-268;
live 5; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 60/041,264
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Bli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/827,208
                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09498809
Patent No. 6242206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6C
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 913 amino acids
amino acid
                                                                                                                                                                 RQAVQRRRQRRPH 605
                                                                                                                                                                                                        901 ROAVORRRORRPH 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.5
Best Local Similarity 87.6
Matches 537; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-498-809-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gaylo, Paul J.
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                               US-09-498-809-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EWSQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EWSOXDLAGPTELLKTOVTKNKLGVLAPSOLORYROELAERARLGYPSCFTNLWALINEA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLHDEPHDHKLSDQREALSHGONPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVR 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLKGLHFHKDYFQHPH 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOANLDKEGVPLLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPH 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSTWKATTLDGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAF 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.5%; Score 2767.5; DB 3; Length 913; 87.6%; Pred. No. 2.7e-268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                           COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/500,358
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                      PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/827,208
FILING DATE: 28-MAR-1997
APPLICATION NUMBER: US 60/014,608
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REGISTRAFION NUMBER: X-10610
REFERENCE TOOKET NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
                                                         United States of America
Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 913 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.6
Matches 537; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                   Indianapolis
                                   Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                     STATE: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-500-358-3
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FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,617 APPLICATION NUMBER: 60/047,618 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,592 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,581 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,587 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,492 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,632 APPLICATION NUMBER: 60/047,601 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,314 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11
APPLICATION WUMBER: 60/043,312
ELING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,313 EARLIER APPLICATION NUMBER: 60/056,893 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,630 APPLICATION NUMBER: 60/047,583 APPLICATION NUMBER: 60/047,500 APPLICATION NUMBER: 60/047,598 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,596 APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-06-06 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 APPLICATION NUMBER: 60/047,503 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/ FILING DATE: 1997-05-23 FILING DATE: 1997-04-11 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 FILING DATE: 1997-04-11 7-05-23 1997-04-11 FILING DATE: 1997-04-1.
APPLICATION NUMBER: 60, FILING DATE: 1997-04-1 FILING DATE: 1997-08-2 FILING DATE: 1997-04 APPLICATION NUMBER: APPLICATION NUMBER: EARLIER I
EARLIER B
EARLIER DE SARLIER DE EARLIER I EARLIER I EARLIER I EARLIER I EARLIER I EARLIER I EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER I EARLIER I EARLIER I EARLIER I EARLIER DEARLIER DEAR EARLIER DE PARLIER DE EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER

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BARLIER APPLICATION NUMBER: 60/057,761
EARLIER PILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER PILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-23
EARLIER FILING DATE: 1997-04-23
EARLIER FILING DATE: 1997-04-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-04-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-23
EARLIER FILING DATE: 1997-04-22
EARLIER FILING DATE: 1997-08-22
                                          EARLIER AFFILIATION NUMBER: 60/056, 662
EARLIER APPLICATION NUMBER: 60/056, 662
EARLIER APPLICATION NUMBER: 60/056, 812
EARLIER FILING DATE: 1997-08-22
EARLIER PELING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,836
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER APPLICATION NUMBER: 60/056,636
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R APPLICATION NUMBER: 60/056,845
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,892
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/047,595
R FILING DATE: 1997-05-23
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,910
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EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,864
APPLICATION NUMBER: 60/056,878
FILING DATE: 1997-08-22
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315 FFWGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP 374 375 ILKIEBPPSTAGRIABPFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG 434 LPNQLTPSEPHICLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQGRFCQ 494 EQGIPFPPISPSEGOLOPRECHTFSDPTCPGAPAVLHF-----SSGVRRTPEE 544 AAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQILEALROAVQRRRQRR 255 SDORBALSHGONPLPIYCALNTKGOSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSE 61 ELLKTOVTKNKLGVLAPSQLORYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL 135 MATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPT Gaps 11; DB 4; Length 483; Indels Score 2509.5; DB 4; Pred. No. 7.3e-243; 2; Mismatches 2; Sequence 209, Application US/09146545
Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1
CURRENT APPLICATION NUMBER: US/09/148,545 EARLIER FILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER PELICATION NUMBER: 60/056,862
EARLIER PELICATION NUMBER: 60/056,887
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-05
FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 n Similarity 96.9%; Conservative PH 605 PH 482 US-09-148-545-209 Query Match Best Local Simi Matches 467; 604 SEQ ID NO 144 495 435 195 RESULT 9 ò ò g ŏ g à g $\dot{\delta}$ qq δ g Š 셤 ð 셤

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CURRENY PILING DATE: 1998-09-04

BARLIER PILING DATE: 1998-03-06

BARLIER PILING DATE: 1999-03-07

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BARLIER PILING DATE: 1997-04-11

BARLIER PELICATION NUMBER: 60/043,674

BARLIER PELICATION NUMBER: 60/043,674

BARLIER APPLICATION NUMBER: 60/043,312

BARLIER PILING DATE: 1997-04-11

BARLIER PILING DATE: 1997-04-11

BARLIER PILING DATE: 1997-04-11

BARLIER FILING DATE: 1997-04-11

BARLIER APPLICATION NUMBER: 60/056,886

BARLIER APPLICATION NUMBER: 60/056,887

BARLIER APPLICATION NUMBER: 60/056,887

BARLIER APPLICATION NUMBER: 60/056,897

BARLIER FILING DATE: 1997-08-22

BARLIER PELING DATE: 1997-08-22

BARLIER APPLICATION NUMBER: 60/056,891

BARLIER PILING DATE: 1997-08-22

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Patent No. 5328842
GENERAL INFORMATION:
APPLICANT: Chiou et al.
TITLE OF INVENTION: COMPOUNDS, VECTORS AND METHODS FOR NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Division/RSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 749;
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19.1%; Score 619; DB 1; I
Best Local Similarity 27.1%; Pred. No. 6.9e-53;
Matches 174; Conservative 125; Mismatches 238;
                                                                                          EQGIPPPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF
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ATTORNEY AGENT INFORMATION:
NAME: JOSEPH A. JONERA
REGISTRATION NUMBER: 26,472
REPERRUCE JOCKET NUMBER: X-8477
TELECOMMUNICATION INFORMATION:
TELECHONE: 317-276-5183
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SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/04
FILING DATE:
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STATE: Indiana
COUNTRY: USA
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Pred. No. 7.3e-243;
2; Mismatches 2;
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EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-66
EARLIER FILING DATE: 1997-06-66
EARLIER FILING DATE: 1997-06-66
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
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EARLIER FILING DATE: 1997-08-22
                                                                           R APPLICATION NUMBER: 60/047,594
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,589
R APPLICATION NUMBER: 60/047,593
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R APPLICATION NUMBER: 60/056,632
R. FILING DATE: 1997-08-22
R. FILING DATE: 1997-08-22
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R. FILING DATE: 1997-08-22
R. FILING DATE: 1997-08-28
R. FILING DATE: 1997-08-28
R. APPLICATION NUMBER: 60/056,881
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,590
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                              FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,576
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APPLICATION NUMBER: 60/047,501
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/056,909
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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Matches 467; Conservative
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                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                   330 CFLEGIWSN----
                                Query Match
Best Local Similarity
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STREET: 87
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US-08-890-615-2
   US-09-045-185-2
                                                              Matches 158;
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                                                                                                               ---ANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLL 376
                                                                                                                                           390 MGVWGSAFSILFNRVLGVSGSQSRGSTMEEEL----ENITTKHIVSNDSSDSDD---- 439
                                                                                                                                                                           ----LLTWRPLAQATHNFLRGLHFH 415
                                                                                                                                                                                                                                         416 KDYFQHP--HFSTWKATTLDGL-----PNQ-----LTPSEPHLCLLDVGYLINTSCL 460
                                                                                                                                                                                                                                                                                                    PLIQPTRDVDLILSLDYNLHGA----FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRE 515
                                                                                                                                                                                                                                                                                                                                                                   ---SSGV-RRIPEEAAAGEVNL-SSSDSPY 558
                                                                                                                                                                                                                                                           500 ISYPLSPLSDFATQDSFDDDELDAAVADPDEFERIYEPLDVKSKKIHVVDSGLTFNLPYP
                                                                                                                                                                                                                                                                                                                       560 LILRPORGVDLIISFDFSARPSDSSPPFKELLLAEKWAKKLPFPKIDPYVFDREGLKE
                                                 ALNTKGOSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kramer, Ruth M.
APPLICANT: Pickard, Richard T.
APPLICANT: Sharp, John D.
APPLICANT: Strifler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
TITLE OF SQUENCES: 3
CORRESPONDEME ADDRESS:
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America
ZIP: 46.28E
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,185
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              559 HYTKVTYSQEDVDKLIHLTHYNVCNNQEQLLEALRQAVQRRRQ
                                                                                                                                                                           KIEEPPSTAGRIA -- EFFTD -------
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NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: P-11369
TELECOMMUNICATION INFORMATION:
TRIEPHONE: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                   CHTFSDPTCP----GAPAVLHF--
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                               EGIWSNLYA-
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387 GLAINTPFPLVLPPTREVHLILSFDFSAGDPFETIRATTDYCRRHKIPFPQVE---EAEL 443
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                                                                                                                                                                                                                                                                                            70 GLLDAVTYLAGVSGSTWAISSLYTNDGDMEALEAD-----LKHRFTRQEW-----DL 116
                                                                                                                                                                                                                                                                                                                                                                              QRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYCA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AKSLOKTIQAARSENYS-LTDFWAYMVISKOTRELPESH-LSNMKKPVEEGTLPYPIFAA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRI 329
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                                                                                                                                                            GYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPISPSPEEQL
                                                                                                                                                                                                                                                        GLLDCVSYITGASGSTWALANLYE----DPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQL
                                                                 Gaps
                                                              Indels 135;
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   Length 541;
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Sequence 2, Application US/08990615
GENERAL INFORMATION:
APPLICANT: Song, Chuanzheng
APPLICANT: Kriz, Ron
APPLICANT: Kriz, Ron
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-GAMMA FITLE OF INVENTION: AND POLYNUCLEOTIDES ENCODING SAME NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
15.4%; Score 498.5; DB 3; 27.8%; Pred. No. 4.9e-41; iive 86; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 TYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
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MEDIUM TYPE: Floppy disk
COMPUTER: TRM PC compatible
COMPUTER: TRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,615
FILING DATE:
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87 CambridgePark Drive
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Best Local Similarity 27.00
Matches 157; Conservative
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LOCATION: (6) ... (242)
NAME/KEY: ACT SITE
LOCATION: (366) ... (535)
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ORGANISM: Homo sapiens
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US-09-246-290A-2
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                                                                                                                                                                                                                                                                                                                                                                     tch 15.2%; Score 490.5; DB 3; al Similarity 27.6%; Pred. No. 3.1e-40; 157; Conservative 86; Mismatches 191;
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US-09-246-290A-2
Sequence 2, Application US/09246290A
Patent No. 6440683
GENERAL INFORMATION:
                                                     REPRENCE/DOCKET NUMBER: GIS3
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-498-4824
TELEFAX: 617-498-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENOTH: 541 antino acids
TYPE: amino acids
          ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                        Active-site
366..535
                                                                                                                                                                                                                                                      NAME/KEY: Active-site LOCATION: 6..242
                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
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CLASSIFICATION:
                                                                                                                                                                                       STRANDEDNESS
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LOCATION:
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Best Local
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APPLICANT: Song, Chuanzheng
APPLICANT: Kriz, Ronald
APPLICANT: Kriz, Ronald
APPLICANT: Kriz, Ronald
APPLICANT: Kriz, Ronald
TITLE OF INVENTION: O'TOSOLIC PHOSPHOLIPASE A2-GAMMA ENZYMES
TITLE OF INVENTION: WID POLYNUCLECTIDES ENCODING SAME
FILE REFERENCE: GFN-5300DV
CURRENT APPLICATION NUMBER: US/09/246,290A
CURRENT FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: US 08/890,615
PRIOR FILING DATE: 1997-07-09
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SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 4, Application US/09687538B

; Patent No. 6514739

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 LORYROELAERARLGYPSCFTNLWA-----LINE--
                                                                                                     APPLICANT: Kauppinen, Markus
APPLICANT: Kauppinen, Markus
TITLE OF INVENTION: Lysophospholipase
TITLE REFERENCE: 5958.210-US
CURRENT APPLICATION NUMBER: US/09/687,538B
CURRENT FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 IPVVAIMATGGGIRAMTSLYGQLAGLKEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Aspergillus niger
US-09-687-5388-4
Udagawa, Hiroaki
                                 Frandsen, Ton
Nielsen, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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TITLE OF INVENTION: Polypeptides Having Lysophospholipase TITLE OF INVENTION: Activity And Nucleic Acids Enocoding Same FILE REFERENCE: 5713.200-US CURRENT APPLICATION NUMBER: US/09/437,687A
                                                                                                                                                   Sequence 2, Application US/09437687A
Patent No. 6489154
GENBRAL INPORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Tony Byun
APPLICANT: Ryoko Itami
APPLICANT: Ryoko Itami
APPLICANT: APA RABALANT: No. 64891541ko Tsutsumi
APPLICANT: Alan Klotz
                                                                                                                                US-09-437-687A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 LPESRIC-----FLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDXEQVPL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GGECVRGFDQFGFVMGTSSSLFNQFLLNNITKIGE------BNDIPS 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 WNTTLIDWW---GRÅL----SYQLIDASEGGPAYTFSSIADTSNFKDADTPFPILVÅD 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 -----LNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 GRAPGQRIVSLNATVYEFNPFEFGTWDPTS-----YG-FAPVEYIGSNFTNGTIEK- 331
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                                                                                                                                                                                                                                                                                                                                     Query Match 6.4%; Score 208; DB 4; L. Best Local Similarity 21.7%; Pred. No. 9.4e-12; Matches 146; Conservative 82; Mismatches 216;
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 09/189,486
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5, 2004, 19:24:58
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Job time: 41.9133 secs
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; Search time 137.133 Seconds (without alignments) 1419.702 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli Sequence 4, Appli	Sequence 638, App Sequence 144, App	Sequence 209, App Sequence 144, App	Sequence 209, App Sequence 6, Appli	Sequence 1, Appli Sequence 1, Appli	Sequence 38, Appl	Sequence 3, Appli	Sequence 50, Appl	Sequence 2, Appli
SUMMARIES	US-10-266-388-2 US-10-266-388-4	US-10-408-765A-638 US-09-981-876-144	US-09-981-876-209 US-09-148-545-144	US-09-148-545-209 US-10-332-426-6	US-10-467-248-1 US-10-380-873B-1	US-10-380-873B-38 US-10-380-873B-22	US-10-332-426-3	US-10-211-462-50	US-10-157-898-2
DB	44	9 6	9	10	16 15	15	12	12	12
% Query Match Length DB	778	1012	483 483	483 1026	996 849	853 854	848	749	749
% Query Match	85.5 85.5	85.5 77.6	77.6	77.6	38.4	35.2	34.4	19.1	19.1
Score	2767.5	2767.5	2509.5 2509.5	2509.5 1492	1243.5	1138	1112	619	619
Result No.	400	w 4	o 10	7	10	11	13	14	15

16	619	19.1	749	13	US-10-062-730-2	Sequence 2, Appli
17	619	19.1	749	14	US-10-021-660-118	Sequence 118, App
18	599.5	18.5	748	12	US-10-157-898-4	
19	490.5	15.2	541	12	US-10-211-462-93	
20	490.5	15.2	541	14	US-10-021-660-127	
21	490.5	15.2	541	16	US-10-741-601-296	
22	490.5	15.2	541	16	US-10-741-601-297	
23	461	14.3	597	14	US-10-181-612-4	
24	419	13.0	180	12	US-10-296-115-917	Sequence 917, App
25	368.5	11.4	261	15	US-10-380-873B-26	Sequence 26, Appl
26	361	11.2	454	15	US-10-380-873B-3	Sequence 3, Appli
27	358	11.1	442	16	US-10-468-519-1	Sequence 1, Appli
28	347.5	10.7	441	16	US-10-468-519-8	
29	344	10.6	445	16	US-10-468-519-5	Sequence 5, Appli
30	339	10.5	384	16	US-10-741-601-295	Sequence 295, App
31	232	7.2	151	14	US-10-017-161-1210	Sequence 1210, Ap
32	232	7.2	151	15	US-10-292-798-1020	
33	220	6.9	150	15	US-10-094-749-1682	Sequence 1682, Ap
34	217	6.7	135	12	US-10-424-599-242280	Sequence 242280,
35	216	6.7	101	15	US-10-094-749-2181	Sequence 2181, Ap
36	211	6.5	137	12	US-10-276-774-1959	Sequence 1959, Ap
37	211	6.5	157	15	US-10-108-260A-4272	Sequence 4272, Ap
38	210	6.5	157	12	US-10-276-774-1940	Sequence 1940, Ap
39	208.5	6.4	137	12	US-10-276-774-1949	Sequence 1949, Ap
40	208.5	6.4	183	0	US-09-989-920-245	Sequence 245, App
41	208.5	6.4	361		US-09-995-494-107	Sequence 107, App
42	208	6.4	97	N	US-10-276-774-2008	Sequence 2008, Ap
43	208	6.4	638	14	US-10-309-437-4	Sequence 4, Appli
44	208	6.4	654	14	US-10-263-250-2	Sequence 2, Appli
45	206	6.4	213	12	US-10-296-115-911	Sequence 911, App

ALIGNMENTS

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RESULT 1
US-10-266-388-2
US-10-266-388-2
Sequence 2, Application US/10266388
Publication No. US20030124702A1
GENERAL INFORMATION:
APPLICANT: KIZ, RON
SONG, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF ENGYMENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: 87 Cambridge Park Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: BADALE FORM:
MEDIUM TYPE: Floppy disk
COMPOTTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT SYSTEM: USA
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/266,388
FILING DATE: 29-Jun-2001
APPLICATION NUMBER: US/09/895,547
FILING DATE: 29-Jun-2001
APPLICATION NUMBER: G15289
FILING DATE: 29-Jun-2001
APPLICATION NUMBER: G15289
TELECOMMUNICATION INFORMATION:
NAME: Brown, Scott A.
REGISTRATION INFORMATION:
NAME: BROWN, SCOTT A.
TELEBENCE, G17) 439-63824
TELEBERAX: G17) 439-63821
INFORMATION FOR SEQ ID NO: 2:
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ZIP: 02140
COMPUTER READABLE FORM:
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CORRESPONDENCES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STREET: MA
COUNTRY: USA
                                                                                                            85.5%; Score 2767.5; DB 14; Length 778;
87.6%; Pred. No. 1.2e-254;
trive 5; Mismatches 22; Indels 49;
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                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                            Sequence 4, Application US/10266388
Publication No. US20030124702A1
GENERAL INFORMATION:
APPLICANT: Kriz, Ron
            LENGTH: 778 amino acids
TYPE: amino acid
                                   STRANDEDNESS: <Unknown>
 CHARACTERISTICS
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                                                                                                       Query Match
Best Local Similarity
Matches 537; Conserv
 SEQUENCE
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US-10-266-388-4
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Pred. No. 1.2e-254;
5; Mismatches 22; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/895,547
FILING DATE: 29-Jun-2001
APPLICATION NUMBER: 09/460,145
FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/266,388
FILING DATE: 07-0ct-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/OCKET NUMBER: G15289
TELECOMMUNICATION INPORMATION:
TELEPHONE: (617) 498-8224
TELEPAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-266-388-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 797 amino acids
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TOPOLOGY: linear
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Best Local Similarity 87.6%;
Matches 537; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS
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534 -SSGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEAL
                                                                                                                                                                                                            Sequence 144, Application US/09981876
Patent No. US20020164669A1
GENERAL INFORMATION:
                                                                                                          1000 ROAVORRRORRPH 1012
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                                                                                                                                                                                                                                     APPLICANT: Ghosh, Sounitra S.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Taylor, Boin D.
APPLICANT: Taylor, Boin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Gary W.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION WHERE: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 638
LENGTH. 1012
LENGTH. 1012
                                                                                                                                                                                      Sequence 638, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
                                                            605
                                                                                           785 ROAVORRRORRPH 797
                                                          RQAVQRRRQRRPH
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; ORGANISM: Homo sapiens
US-10-408-765A-638
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940 SAPGVRRTPEEAAAGEVNLSSSDSPYHYTKVTYSOEDVDKLLHLTHYNVCNNOEOLLEAL 999
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1997-08-22

NUMBER: 60/047,596 1997-05-23 1997-05-23 NUMBER: 60/047,632 1997-05-23 NUMBER: 60/047,601 1997-05-23 NUMBER: 60/047,601 1997-04-11 NUMBER: 60/043,568 1997-04-11 NUMBER: 60/043,568	RE 60/043, 56, 104-11, 56, 104	
APPLICATION FILING DATE. APPLICATION APPLICATION APPLICATION APPLICATION FILING DATE.	PELICATION DATE PELICATION DAT	PELLING DATE
PRIOR		PRIOR

| PRIOR APPLICATION NUMBER: 60056, 615
| PRIOR APPLICATION NUMBER: 60057, 701
| PRIOR APPLICATION NUMBER: 60057, 701
| PRIOR APPLICATION NUMBER: 60057, 701
| PRIOR PLING DATE: 1997-62, 2047, 526
| PRIOR PLING DATE: 1997-62, 2047, 526
| PRIOR PLING DATE: 1997-62, 2047, 526
| PRIOR PRIOR CALLON NUMBER: 60047, 526
| PRIOR PRIOR PAPEL CALLON NUMBER: 60047, 526
| PRIOR PRIOR PRING DATE: 1997-62, 2047, 526
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| PRIOR PRING DATE: 1997-62, 2047, 531
| PRIOR PRING DATE: 1997-62, 2041
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FILING DATE:
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                                                          SDQREALSHGONDLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSE
                                                                                                                                                                                                                                                              FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP
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                                                                                                                                        SDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSE
                                                                                                                                                                                                                                                                                                                  FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP
                                                                                                                                                                                                                                                                                                                                                                                LLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                     241 LLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG
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                        ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL
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Fatent No. US20020164669A1

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: 70 Human Secreted Proteins

FILE REFERENCE: P2001P1

CURRENT APPLICATION NUMBER: US/09/981,876

CURRENT FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: 09/148,545

PRIOR FILING DATE: 1999-09-04

PRIOR APPLICATION NUMBER: 60/040,162

PRIOR FILING DATE: 1997-03-07

PRIOR PILING DATE: 1997-03-07

PRIOR PILING DATE: 1997-03-07

PRIOR FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,633
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,671
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,674
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,669
FILING DATE: 1997-04-11
PILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,617
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,598
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
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APPLICATION NUMBER: 60/056,662
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,587
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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LING DATE: 1997-05-23
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LING DATE: 1997-04-11
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FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/048,974
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APPLICATION NUMBER: 60/056,886
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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181 FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP 240 241 LLKIEEPPSTAGRIABFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG 300 603 135 MATGGGIRAMISLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPT 194 254 61 ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL 120 434 LPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQ 494 421 AAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRR 480 SDOREALSHGONPLPIYCALNTKGOSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSE FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP LLKIEEPPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDG ---SSGVRRTPEE AAAGEVNLSSSDSPYHYTKVTYSQEDVDKLI.HLTHYNVCNNQEQLLEALRQAVQRRRQRR ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKL 1 MATGGGIRAMISLYGQLAGLKELGLLDCXSYITGASGSTWALANLYKDPEWSQKDLAGPT Gaps 11; Length 483; Indels EQGIPFPPISPSPEEQLOPRECHTFSDPTCPGAPAVLHF-----DB 9; Score 2509.5; DB 9; Pred. No. 2.4e-230; 2; Mismatches 2; Sequence 144, Application US/09148545
Publication No. US20030027132A1
GENERAL INFORMATION:
APPLICANT: Rosen te al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1 CURRENT APPLICATION NUMBER: US/09/148,545 CURRENT FILING DATE: 1998-09-04 EARLIER APPLICATION NUMBER: PCT/US98/04482 BARLIER FILING DATE: 1998-03-06 EARLIER APPLICATION NUMBER: 66/040,162 BARLIER FILING DATE: 1997-03-07 PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,862
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,887
PRIOR APPLICATION NUMBER: 60/056,908
PRIOR PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,908
PRIOR FILING DATE: 1997-08-22
PRIOR PRILING DATE: 1997-08-05
PRIOR FILING DATE: 1997-0-05
SOFTWARRE: PALENTING NUMBER: 60/056,884
PRIOR FILING DATE: 1997-0-05
SOFTWARRE: PALENTING NUMBER: 00/056,884
PRIOR FILING DATE: 1997-0-05-05
SOFTWARRE: PALENTING NUMBER: 00/056,884
PRIOR FILING DATE: 1997-08-22 Query Match
Best Local Similarity 96.9%;
Matches 467; Conservative PH 605 PH 482 RESULT 6 US-09-148-545-144 544 195 255 315 375 435 301 495 361 604 481 LENGTH: ò g δ g ò ద $\dot{\delta}$ g Š g Š d ð g δ _업 Š

60/040,333 60/038,621 60/040,161 60/040,626 60/040,334 60/040,336 60/040,336 60/040,163 60/047,615	-23 60/047,597 -23 60/047,633 -23 60/047,633 60/047,617 -23 60/047,618 60/047,518 60/047,592 60/047,592 60/047,592 60/047,592 60/047,592	23,00,047,4 20,00,047,5 20,00,047,5 20,00,047,5 20,00,047,6 20,00,043,5 20,00,043,5 20,00,043,5 20,00,043,6
NUMBER: 1997-03 NUMBER: 1997-05 NUMBER: 1997-0	1997-05 NUMBER:	1997-05 NUMBER: 1997-04 NUMBER: 1997-04 NUMBER: 1997-04 NUMBER: 1997-04 NUMBER: 1997-04 NUMBER: 1997-04 NUMBER:
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BARLIER FILING DATE: 1997-06-22
BARLIER FILING DATE: 1997-06-25
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BARLIER FILING DATE: 1997-06-22
BARLIER FILING DATE: 19

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361 EQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHFPLVSDSFREYSAPGVRRTPEE 420
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TITLE OF INVENTION: 70 Human Secreted Proteins
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EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-07
EARLIER FILING DATE: 1997-03-07
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CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
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EARLIER APPLICATION NUMBER: 60/040,163
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER PILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER PILING DATE: 1997-05-23
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R FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,592
TITING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,617
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APPLICATION NUMBER: 60/047,618
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FILING DATE: 1997-05-23
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FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/047,633
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Pred. No. 2.4e-230;
2; Mismatches 2; Indels 11;
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EARLIER APPLICATION NUMBER: 60/048,964
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER APPLICATION NUMBER: 80/056,884
EARLIER PELENG DATE: 1997-08-22
SOFTWARE: PACENTIN VET: 2.0
APPLICATION NUMBER: 60/04/,500
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,593
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APPLICATION NUMBER: 60/056,887
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,875
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APPLICATION WUMBER: 60/047,614
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
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APPLICATION NUMBER: 60/043,576
FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/056,632
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APPLICATION NUMBER: 60/056,664
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,876
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APPLICATION NUMBER: 60/056,881
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,862
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Best Local Similarity 96.9%;
Matches 467; Conservative
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EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-04-11
EARLIER PELING DATE: 1997-04-11
EARLIER PELING DATE: 1997-04-11
EARLIER PELING DATE: 1997-04-11
EARLIER PELING DATE: 1997-06-22
EARLIER PELING DATE: 1997-06-22
EARLIER PELING DATE: 1997-06-22
EARLIER PELING DATE: 1997-08-22
EARLIER PELING DATE: 19 ER FILING DATE: 1997-08-22
ER APPLICATION WUMBER: 60/056,864
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,631
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,845
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,892
ER FILING DATE: 1997-08-23
ER APPLICATION NUMBER: 60/057,761
ER PELLING DATE: 05-SEP-1997
ER PELLING DATE: 05-SEP-1997
ER PELLING DATE: 05-SEP-1997 R FILING DATE: 1997-05-23

RR APPLICATION NUMBER: 60/047,588

RR FILING DATE: 1997-05-23

RR APPLICATION NUMBER: 60/047,585

RR FILING DATE: 1997-05-23

RR APPLICATION NUMBER: 60/047,586 EARLIER APPLICATION NUMBER. C., EARLIER PILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,590 EARLIER FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER: 60/047,594 BARLIER BARLIE

135 MATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPT 194

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Query Match 77.6%; Score 2509.5; DB 10; Length 483; Best Local Similarity 96.9%; Pred. No. 2.4e-230; Matches 467; Conservative 2; Mismatches 2; Indels 11;

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NAME/KEY: misc_feature
) OTHER INFORMATION: Incyte ID No. US20040029136A1 7477093CD1
US-10-332-426-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10467248 Publication No. US20040086905A1 GENERAL INFORMATION:
                                                                                     46.1%;
51.6%;
                                                                                     Query Match
Best Local Similarity 51.6%
Matches 296; Conservative
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US-10-467-248-1
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FFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVP
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                                                                                                                          SDOREALSHGONPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSE
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GENERAL INCORMETION:
APPLICANT: AZIMZAI, Yalda; DAS, Debopriya;
APPLICANT: THORYTEN
APPLICANT: THORYTON, Michael, IJ, Dyung Alna M.;
APPLICANT: THORYTON, Michael, IJ, Dyung Alna M.;
APPLICANT: GANDHI, Ameena R.; CHAMLA, Narinder K.;
APPLICANT: KHAN, Farrah A.; LU, Yan,
APPLICANT: YAO, Monique G.; HAFALIA, April J. A.;
APPLICANT: YAO, Monique G.; HAFALIA, April J. A.;
APPLICANT: YAO, Monique G.; HAFALIA, April J. A.;
APPLICANT: YOO, Monique G.; HAFALIA, April J. A.;
APPLICANT: YOO, Monique G.; HAFALIA, April J. A.;
APPLICANT: YOO, Monique G.; HAFALIA, April J. A.;
APPLICANT: YOU'REN Danniel B.; BAUGHN, Mariah R.
TITLE OF INVENTION: LIPID METABOLISM MOLECULES
FILE REFERENCE: PLO152 USN
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US 60/216,801
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,801
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/220,739
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/220,739
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/220,739
PRIOR APPLICATION NUMBER: US 60/220,739
PRIOR APPLICATION NUMBER: US 60/220,739
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NUMBER OF SEQ ID NOS: 16
SOFTWARE: PERL PROGRAM
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              868 FRPGRRIDLIISFDYSLSAPFBALQQTELYCRARGLPFPRVEPSPQDQHQPRECHLFSDP 927
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                                                                                                                                                           LPLTIGKEVTMDVPAPNAPGVRLQLKAEGCPEELAVHLGFNLCAEEQAFLSRRKQVVAK
                                                                                                                                                                                                                                                       LOPPPLGFKRFSCLSLPSSWDYRLR-----BLAVRLGFGPCAEEQAFLSRRKQVVAA
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                                                            Gaps
                                                            34;
  Length 1026;
                                                         Indels
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APPLICANT: ARVIZU, Chandra S.; BAUGHN, Mariah R.;
APPLICANT: LU, Yan; HAFALIA, April J.A.;
APPLICANT: CHAWLA, Narinder K.; GRIFFIN, Jennifer A.;
APPLICANT: LU, Poyung Alia M.; YUE, Henry;
APPLICANT: DING, Li, ELLIOTT, VICK; S.;
APPLICANT: FORSYTHE, Ian J.; RAMKUMAR, Jayalaxmi;
APPLICANT: GANDHI, Ameena R.; ISON, CarigH H.;
APPLICANT: ARREN, Bridget A.; TANG, Y. TOM;
APPLICANT: EMERLING, Brocke M.; HONCHELL, Cynthia D.;
; Score 1492; DB 12;
; Pred. No. 1.3e-132;
92; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 KLLHLTHYNVCNNQEQLLEALRQAVQRRR-QRRP 604
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                                                                                                                                                                                                                                                                                                    tch 38.4%; Score 1243.5; DB 16; Length 996; al Similarity 44.8%; Pred. No. 6.6e-109; 261; Conservative 86; Mismatches 187; Indels 49;
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                                                                                                                                                                                                                                                                                                                                                          56 RDLGSLQPPPLGFKRFSCLS-----LPSSWDYRL-
                                                                                                                                                                                                                                     FEATURE:
NAME/KEX: misc feature
OTHER INFORMATION: Incyte ID No: 7472774CD1
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: US 60/276,891
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-18
PRIOR PILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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Best Local S
Matches 261
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TITLE OF INVENTION: Polypeptide having phospholipase A2 activity FILE REFERENCE: 2139.34
CURRENT APPLICATION NUMBER: US/10/380,873B
CURRENT APPLICATION NUMBER: US/09.873B
PRIOR APPLICATION NUMBER: JP 00/146466
PRIOR APPLICATION NUMBER: JP 00/146466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 15; Length 849;
TITLE OF INVENTION: Polypeptide having phospholipase A2 FILE REFERENCE: 2139.34
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                                                CURRENT APPLICATION NUMBER: US/10/380,873B
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: PD 00/146466
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
SEQ ID NO 1
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, Sequence 38, Application US/10380873B
, Publication No. US20040014089A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 41.8
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                             849
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844

Sequence 1, Application US/10380873B Publication No. US20040014089A1 GENERAL INFORMATION: APPLICANT: Hiromasa MIYAJI, et al.

RESULT 10 US-10-380-873B-1

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86 ELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRAMT 145
                                                                                                                                                                                                                                                                SLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTKNK 205
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                                                                                                                                                                                  Gaps
                                                                                                                                                                               28;
                                                                                                                        Length 854;
                                                                                                                     tch 34.8%; Score 1127; DB 15; Length al Similarity 42.6%; Pred. No. 7e-98; 231; Conservative 100; Mismatches 183; Indels
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APPLICANT: AZIMZAI, Yalda; DAS, Debopriya;
APPLICANT: THORNTON, Michael, IuU, Dyung Ahna M.;
APPLICANT: TRIBOULEY, Catherine M.; VUE, Henry;
APPLICANT: GANDHI, Ameena R.; CHAMIA, Narinder K.;
APPLICANT: KHAN, Farrah A.; LU, Yan;
APPLICANT: ELLOTT, VICK! S.; ARVIZU, Chandra S.;
APPLICANT: ELLOTT, VICK! S.; ARVIZU, Chandra S.;
APPLICANT: LAL, Preet; RAMKUMAR, Jayalaxmi;
APPLICANT: NOUYEN, Danniel B.; BAUGHN, Mariah R.;
TITLE OF INVENTION: LIFID METABOLISM MOLECULES
FILE REFERENCE: PI-0152 USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/332,426
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US 60/216,803
PRIOR FILING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
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                                     ; ORGANISM: Mus musculus US-10-380-873B-22
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| PKLRKQDPTRLPTRLPTRPMSSFSQAVLDIFTSRITCAQTFNFTRGLCMYKDYTARKDFVV 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               653 SEDAWHSHNYGYPDACPNQLTPMKDFLSLVDGGFAINSPFFLVLQPQRAVDLIVSFDYSL
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                                                                                                                                                                                                                                                                                                                                          Gaps
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FORDILL SEQUENCE SE
                                                                                                                                                                                                                                                                                    Length 853;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                           Query Match 35.2%; Score 1138; DB 15; Best Local Similarity 42.4%; Pred. No. 6.2e-99; Matches 235; Conservative 102; Mismatches 189;
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PRIOR APPLICATION NUMBER: JP 00/146466;
PRIOR FILING DATE: 2000-09-19;
PRIOR FILING DATE: 2000-09-19;
PRIOR FILING DATE: 2001-05-16;
NUMBER OF SEQ ID NOS: 47;
SEQ ID NO 22;
LENGTH: 854
        01/284044
PRIOR APPLICATION NUMBER: JP 0
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
LENGTH: 853
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                                                                                                                                                                                             ORGANISM: Mus musculus
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US-10-380-873B-22
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RESULT 15
US-10-157-898-2
; Sequence 2, Application US/10157898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GONDLDIYCALNIKGOSLITFEFGEMCEFSPYBVGFPKYGAFIPSELFGSEFFMGQLMKR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 GQNPYPIYTSVAVR-TNLSGEDFA-WCEFTPYKVGFPKYGAYVPTELFGSELFMGRLLQL 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 MTSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 NKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSH 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 LPESRIÇFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANL-DKEQVPLLKIEEPP 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605 RLRTRLLTPQGPFSQAVLDIFTSRFTSAQSFNFTRGLCLHKDYVAGREFVAWKDTHPDAF 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 PNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLGRFCQE 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496 QGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF-----SSGV-RRTPEE 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 MĒLLAAVQSGPSAELEAQTSKLGEGGILLSSLPLG-QBEQCSVALGEGEGVALSMTVEMS 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----STAGRIAEFFIDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKAITLDGL
                                                                                                                                                                                                                                                                                                                                                              43 MESLSVAQAG-----VQWRDLGS----LQPPPLGFKRFSC-----LSLPSSWDYR
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc feature
TOTHER INFORMATION: Incyte ID No. US20040029136A1 1281946CD1
US-10-332-426-3
                                                                                                                                                                                                                                                                                             Query Match 34.4%; Score 1112; DB 12; Length Best Local Similarity 41.2%; Pred. No. 1.9e-96; Matches 247; Conservative 97; Mismatches 211; Indels
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/220,046
PRIOR FILING DATE: 2000-07-21
PRIOR PAPLICATION NUMBER: US 60/220,739
PRIOR PILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PERL Program
SOFTWARE: PERL Program
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US-10-211-462-50
Sequence 50, Application US/10211462
Publication No. US20040033495A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Murray, Richard
APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Aziz, Natasha
APPLICANT: Eos Biotechnology, Inc.
                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                              LENGTH: 848
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TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators FILE REFERENCE: 018501-006200US
CURRENT APPLICATION NUMBER: US/10/211,462
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US 09/784,356
PRIOR PILING DATE: 2001-02-13
PRIOR PILING DATE: 2001-02-14
PRIOR PILING DATE: 2001-02-15
PRIOR PELING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 SGILDCATYVAGLSGSTWYMSTLYSHPDFPEK---GPERINEELMKNVSHNPLLLLTPQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 KDYFQHP--HFSTWKATTLDGL-----PNQ-----LTPSEPHLCLLDVGYLINTSCL
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Publication No. US20030225011A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DAVID, Samuel
APPLICANT: DAVID, Samuel
APPLICANT: EALYAS, Athena
TITLE OF INVENTION: PHOSPHOLIPASE AZ EXPRESSION AND ACTIVITY AND USE THEREOF FOR DIAC
TITLE OF INVENTION: PROGNOSITCATION PREVENTION AND TREATMENT OF NEURAL INFLAMMATORY
TITLE OF INVENTION: DEMYELINATING DISEASE
CURRENT APPLICATION NUMBER: US/10/157,898
CURRENT PILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 749
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19.1%; Score 619; DB 12; Length 749;
Best Local Similarity 27.1%; Pred. No. 1.9e-49;
Matches 174; Conservative 125; Mismatches 238; Indels 106
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ORGANISM: Homo sapiens
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5, 2004, 19:41:16

Search completed: October Job time: 141.133 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

5, 2004, 19:21:45; Search time 41.14 Seconds (without alignments) 1414.581 Million cell updates/sec October Run on:

US-09-830-321A-2 3235 Title: Perfect score:

1 MIFVELSPTLALCLERVASH........EQLLEALRQAVQRRRQRRPH 605 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:* Database :

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Length	444 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
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Score	6 1 9 8 8 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9	
Result No.	11111111111111111111111111111111111111	

protein F1L3.20 [i	probable polyketid	oxidoreductase, sh	exodeoxyribonuclea	actinomycin synthe	v-type ATP synthas	plectin - rat	decay-accelerating	pol polyprotein -	Glucosamine-fructo	hypothetical prote	qene LL5 protein -	protein-tyrosine k	[heparan sulfate]-	probable membrane	hypothetical prote
D86311	B70588	B82181	G81751	T14591	D75487	A39638	A26359	GNLJGA	AD1079	T39102	S37032	TVFVF	A49733	C86934	AC2962
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101	100.5	100	99.5	99.5	56	o	98.	97	σ	6	ማ	σ	σ	95.	95.5

ALIGNMENTS

REGULT 1 A39229 A39229 phospholipase A2 (EC 3.1.1.4), cytosolic - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 1.0-Sep-1999 #sequence revision 10-Sep-1999 #text_change 20-Apr-2000 C;Date: 1.0-Sep-1999 #sequence revision 10-Sep-1999 #text_change 20-Apr-2000 C;Accession: A39329, A39898; A54198; S68898 R;Sharp, J.D.; White, D.L.; Chiou, X.G.; Goodson, T.; Gamboa, G.C.; McClure, D.; Burgett, J. Biol. Chem. 266, 14850-14853, 1991 A;Title: Molecular cloning and expression of human Ca(2+)-sensitive cytosolic phospholippa, A;Title: Molecular cloning and expression of human Ca(2+)-sensitive cytosolic phospholippa, A;Reference number: A39329; MUID:91331987; PMID:1869522
A; Accession: A39329 A; Accession: A39329 A; Accession: A39329 A; Accession: A39898 A; Molecule type: mRNA

A;Residues: 1-749 <CLA>
A;Cross-references: GB:M72393; NID:g190006; PIDN:AAB00789.1; PID:g190007
A;Note: part of this sequence was confirmed by protein sequencing
R;Li, B.; Copp, L.; Castelhano, A.L.; Feng, R.; Stahl, M.; Yuan, Z.; Krantz, A.
Biochemistry 33, 8594-8603, 1994
A;Title: Inactivation of a cytosolic phospholipase A-2 by thiol-modifying reagents: cyste
A;Reference number: A54198; MUID:94304876; PMID:8031794

A Accession: A54198
A Molecule type: protein
A Rolecule type: protein
A;Residues: 319-338, X',340-345, X',347-358 «LIA»
A;Residues: 319-338, X',340-345, X',347-358 «LIA»
A;Residues: 319-338, X',340-345, X',347-358 «LIA»
A;Residues: 318-338, X',340-345, X',347-358 «LIA»
A;Rocton, R.D.; Leighton, I.A.; Campbell, D.G.; Cohen, P.; Creaney, A.; Wilton, D.C.; Mas Eur. J. Biochem. 238, 690-697, 1996
A;Title: Cloning and expression of cytosolic phospholipase A(2) (cPLA(2)) and a naturally esults in an increase in specific activity.
A;Reference number: S68897; MUID:96300233; PMID:8706669

A;Molecule type: protein A;Residues: 497-507 <GOR> C;Comment: This cytosolic phospholipase A2 translocates to membrane vesicles in response C; Genetics:

A; Gene: GDB: PLA2G4A; PLA2G4

A,Cross-references: GDB:134687; OMIM:600522
A;Map position: 1q25-1q25
C;Superfamily: cytosolic phospholipase A2
C;Keywords: calcium; carboxylic ester bydrolase; cytosol; inflammation; phosphoprotein F;505/Binding site: phosphate (Ser) (covalent) #status experimental

22; Gaps Query Match
19.1%; Score 619; DB 1; Length 749;
Best Local Similarity 27.1%; Pred. No. 1.1e-39;
Matches 174; Conservative 125; Mismatches 238; Indels 106;

```
cytosolic phospholipase A2 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: 150699
R;Malefski, E.A.; Sultzman, L.A.; Martin, D.M.; Kriz, R.W.; Towler, P.S.; Knopf, J.L.; C. B. Biol. Chem. 269, 18239-18249, 1994
A;Title: Delineation of two functionally distinct domains of cytosolic phospholipase A2, A;Reference number: A54908; MUID:94299545; PMID:8027085
A;Accession: 150699
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
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272 VKRYVESLWKKKSSGQPVTFTDIFGMLIGETLIQNR-MSMTLSSLKEKVNAARCPLPLFT 330
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                                                                                                                                               214 LORYROBLAERARLGYPSCFINLWA-LINEALLHDEPHDHKLSDOREALSHGONPLPIYC 272
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LGLLDCVSYITGASGSTWALANLYEDPEWSOKDLAGPTEL---LKTQVTKNKLGVLAPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 -HFSTWKATTLDGL-----PNQ-----LTPSEPHLCLLDVGYLINTSCLPLLQPTRD
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A;Cross-references: EMBL:U10329; NID:g508624; PIDN:AAA53228.1; PID:g508625 C;Superfamily: oytosolic phospholipase A2 C;Keywords: cytosol
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Matches 166; Conserval
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C;Species: Mus musculus (house mouse)
C;Accession: B39898
R;Clark, J.D.; Lin, L.L.; Kriz, R.W.; Ramesha, C.S.; Sultzman, L.A.; Lin, A.Y.; Milona, Cell 65, 1043-1051, 1991
A;Clark, J.D.; Lin, L.L.; Kriz, R.W.; Ramesha, C.S.; Sultzman, L.A.; Lin, A.Y.; Milona, Cell 65, 1043-1051, 1991
A;Reference number: A39898; MUD:91256305; PMID:1904318
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A;Residues: 1-749 < CLA>
A;Cross-references: GB:M7294
A;Cross-references: GB:M7294
C;Comment: This cytosolic phospholipase A2 translocates to membrane vesicles in response C;Superfamily: cytosolic phospholipase A2
C;Keywords: calcium; carboxylic ester hydrolase; cytosol; inflammation
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                                                                                                                                                                                                                                                                                                       272 VKRYVESLWKKKSSGQPVTFTDIFGMLIGETLIHNRMNT-TLSSLKEKVNTAQCPLPLFT 330
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                                                                                                              QAFLSRRKQVVAAALRQAL---QLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKE 156
                                                                                                                                                                                                157 LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAPSQ
                                                                                                                                                                                                                        LORYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDOREALSHGONPLPIYC
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                            ESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRELA----VRLGFGPCAEE
                                                                                                                                                                                                                                                                                                                                                                   ALNIKGOSLITFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL
                                                                  ETLGTATFTVSSMKVGEKKEVPFIFNQVTEMVLEMS----LEVCSCPDLRFSMALCDQE
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.larity 27.1%; Pred. No. 2.3e-38;
Conservative 126; Mismatches 247; Indels
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Matches 172; Conserv
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R.Pickard, R.T.; Strifler, B.A.; Kramer, R.M.; Sharp, J.D.
R.Pickard, R.T.; Strifler, B.A.; Kramer, R.M.; Sharp, J.D.
R.Pickard, R.T.; Strifler, B.A.; Kramer, R.M.; Sharp, J.D.
A;Title: Molecular cloning of two new human paralogs of 85-kDa cytosolic phospholipase A;
A;Reference number: Z17618; MUID:99185108; PMID:10085124
A;Reference number: Z17618; MUID:99185108; PMID:10085124
A;Reference number: Z17618; MUID:99185108; PMID:10085124
A;Reference number: RMA
A;Residues: 1-541 < Protein RMA
A;Residues: 1-541 < Protein Sequence Database, May 1999
A;Reference number: Z16472
A;Reference number: Z16472
A;Residues: 443-541 < ANS>
A;Residues: 443-541 < ANS>
A;Residues: 443-541 < ANS>
A;Residues: A43-541 < ANS>
A;Residues: A43-541 < ANS>
A;Residues: A43-541 < ANS>
A;Residues: A43-541 < ANS>
A;Residues: EMBL:ALOS093
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373 VKQYEENPLHFLMGVWGSAFSILFNRVLGVKETTSSSTMEEELEQIKPEHIVGDDSADNE 432
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C.Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
                                                      366 ANLDK---EQVPLLKIEEPPSTAGRIAEFFTDLL-----TWRPLAQATHNFLRGLHFH
                                                                                                                  EETQRGGTESADAEDERORHAQASWVQRMLTSIMGDTTLFTTREGRAGKVHNFMLGLNLN
                                                                                                                                                                                                            STLPFSPFSGITHQTSLEEEVDAVIDPDEFERIYEPLDVKSKKIHVVDSGLTFNLPYPLI
                                                                                                                                                                                                                                                                                                                           TF----SDPTCPGAPAVLHF------SSGV-RRTPEEAAAGEVNL-SSSDSPYHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                        416 KDYFQHPHFSTWKATTLDGLPNQLT-PSE-----
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Note: DKFZp586C0423.1
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A,Map position: 19
A,Note: DKFZp586C04;
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C;Species: Brachydanio rerio (zebra fish)
C;Species: Brachydanio rerio (zebra fish)
C;Species: Brachydanio rerio (zebra fish)
C;Accession: B54908
R;Malefski, E.A.; Sultzman, L.A.; Martin, D.M.; Kriz, R.W.; Towler, P.S.; Knopf, J.L.; C
J. Biol. Chem. 269, 18239-18249, 1994
J. Biol. Chem. 269, 18239-18249, 1994
J.Yithle: Delineation of two functionally distinct domains of cytosolic phospholipase A2, A;Reference number: A54908; MUID:94299545; PMID:8027085
A;Recession: B54908
A;Recession: B54908
A;Residues: 1-741 cMAL2>
A;Residues: 1-741 cMAL2>
A;Cross_references: EMB:U1029
C;Superfamily: cytosolic phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                   336
                                                                                                                                                                  337 SNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKI-------EEP 381
                                                                                                                                                                                                                                                                                                394 GSAFSILFNRVLGVSNS------QNKGPTMEEELENIRLKHLVSNDSSDSEDESQHP 444
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                     218 RQELAERARLGYPSCFINLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNT 276
                                                                                                                                                                                                                                                                                                                                                                     ----EFFTDLL------TWRPLAQATHNFLRGLHFHKDYFQ 420
                                                                                                                                                                                                                                                                                                                                                                                                               445 KGTENSEANEEYQNSSQESWVQRMLMALVGDSALFNTREGRAGKVHNFMLGLNLNSCYPL 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466 TRDVDLILSLDYNLHGA-----FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTF- 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SDPTCPGAPAVLHF------SSGV-RRIPERAAAGEVNL-SSSDSPYHYT 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | | ::|; | ::|; | EKDTSSEKDC---PTIIHFVLANINFRKYKAPGLPRESKEEKDFADFDIFDDPNTPFSTF 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AANLQDSLYWASEPSQFWDRWVRNQ 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 TSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.7%; Score 572; DB 2;
larity 26.5%; Pred. No. 4.8e-36;
Conservative 115; Mismatches 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115; Mismatches
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probable lysophospholipase (EC 3.1.1.5) precursor SPAC977.09c [similarity] - fission yea
C,Species: Schizosaccharomyces pombe
C,Species: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference Language 1 52023 A; Reference Language 1 52023 A; Residues: translated from GB/EMBL/DDBJ A; Status: translated from GB/EMBL/DDBJ A; Status: translated from GB/EMBL/DDBJ A; Status: translated from GB/EMBL/DDBJ A; Residues: 1-673 < ZINA A; Residues: 1-673 < ZINA A; Residues: 1-673 < ZINA A; Residues: EMBL:AL137130; NID:96742151; PIDN:CAB69631.1; PID:96742159; GSPDB:GN A; Cross-references: Errain 972h(-); Cosmid C977 R; Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H. B; Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H. B; Yoshioka, S.; Kato, R.; Nation of open reading frames in Schizosaccharomyces pombe cDNAs. A; Reference number: Z17323; MUID:98162722; PMID:9501991 A; Reference number: Z17323; MUID:98162722; PMID:9501991 A; Residues: 427-673 < YOS> A; Residues: BMBL:DB9183; NID:91749573; PIDN:BAA13845.1; PID:91749574 A; Reperimental Bource: Extrain PR745 A; Reperimental Bource: Strain PR745 A; Reperimental Bource: Stra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKRKPALVKRSTDASYAPFNVTCSNDNLLRPASEGLNEG----EQSYINKRISKVNSELR 108
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                                                                                                                                                                                                                                                                                                                                        311 FFFFFFFFFSHSVTQAGVQWRDLGSLQAPPPGFWPFSCLSLLRTWDYRRPHHAQLIFCIFS 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T50281; T42738
R;Zimmermann, W.; Wambutt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell,
submitted to the EMBL Data Library, January 2000
A;Reference number: Z25053
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                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                               37 FFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRELA-
                                                                                                                                           Length 613;
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                                                                                                                                                                                                               Indels
                                                                                                                                       Score 193.5; DB 4;
Pred. No. 7.3e-07;
1; Mismatches 17;
                                                                                                                                              6.0%;
                                                                                                                                                                                                                  42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 RNGVLPC 377
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                                                                                                                                              Query Match
Best Local Similarity
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C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C;Accession: C40201
Personal communication, 1992
A;Claverie, J.W.
A;Reference number: A40201
A;Molecule type: DNA
A;Residues: 1-613 <CLA>
A;Residues: 1-613 <CLA>
A;Residues: J. 638-841, 1992
A;Title: Identifying coding exons by similarity search: Alu-derived and other potentiall
A;Recension: C40201
A;Residues: A40200; WUID:92241891; PMID:1572661
A;Residues: J. 638-841, 1992
A;Title: Identifying coding exons by similarity search: Alu-derived and other potentiall
A;Reference number: A40200; WUID:92241891; PMID:1572661
A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation in all 6 reading frames of d
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Cipate: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
Cipate: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
Cipacesion: A40201
Cipacesion: A40201
Airitale: Communication, 1992
Airitale: Lyoe: DNA
Airitale: Locatifying coding exons by similarity search: Alu-derived and other potentiall Airitale: Identifying coding exons by similarity search: Alu-derived and other potentiall Airitale: Identifying coding exons by similarity search: Alu-derived and other potentiall Airitale: Identifying coding exons by similarity search: Alu-derived and other potentiall Airitale: Identifying coding exons by similarity search: Alu-derived and other potentiall Airitale: Identifying coding exons by similarity is a conceptual translation in all 6 reading frames of cipacement: This "warning" entry is a conceptual translation in all 6 reading frames of cipacement: Any significant similarity of a predicted protein sequence to a portion of the
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                     451
                                                                                                                                                                                                                                                                                                                                                                                                                                        444 DLWSKAPASCYILKGET----GPVVWHF------PLFNIDACGGDIEAWSDTYDTFKLAD 493
                                                                                                                                                             293 GEHPPPEDEGGEPEHTWLTEMLENWTR--TSLEKQEQP----HEDPERKGSLSNLMDFVK 346
                                                                                                                                                                                                                                                                                                        Q----PRECHTFSDPTCPGAPAVLHFSSGVRRTP---EEAAAGEVNLSSSDSPYHYTKV 563
                                                                                                                     W-----ASEPSOFW----DRWVRNOANLDKEOVPLLKIEEPPSTAGRIAEFF----
                                                                                                                                                                                                                                                             -TOLLIWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNOLTPSEPHLCLLDV
                                                                                                                                                                                                                                                                                                                                                                                              GYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPISPSEEQL
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80.9%; Pred. No. 3.4e-07;
ative 1; Mismatches 8; Indels
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Matches 38; Conserv
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272 306 323 358 367 417 447 524 492 568	1.2002 1.2002 1.2002 1.2004 1.2	31; 143 116 179 176 230 234 279 280
Db 222 NYYNDLRKEIDOKKHAGFDCSLTDLWGRALSRKLVDAERGGPGITYSSMRN 261LSHGONPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFFKYGAFI Db 273 OSWFQNADYPPIVADSRLEEETAIPANTSIFEFTAYEFGTWDNGIKAFI OY 307 PSELFGSEFFMGQLMKRLEESRICFIEGHWSNLYAANLQDSLYWASEPSQFW Db 324 PMEYVGTHLDGVPPDKSCIHNYDNAGFVMGTSATLFNSFLLD	RESULT 9 S66633 hypothetical protein YOL011w - yeast (Saccharomyces cerevisiae) NyAlternate names: hypothetical protein 02349 C;Species: Saccharomyces cerevisiae C;Date: 12-0u1-1996 #sequence_revision 12-0u1-1996 #text_change 19-Apr-2002 C;Accession: S6663 E; Pohl, T.M. submitted to the Protein Sequence Database, July 1996 A;Reference number: S66685 A;Accession: S6685 A;Accession: S6685 A;Accession: S6685 A;Accession: S6685 A;Accession: S6685 A;Accession: S6685 A;Accession: S6886 A;Accession: S6	14; IMATG IMATG IMATG IMATG IMGRA IMGRA IMGRA IMGRA IMGRA IMGRA IDGRYF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 VREASGLSDNETEWLKKRDAYTKEALHSFLNRATSNFSDTSLLSTLFGSNSSNMPKIAVA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| ::
-----TDLPSF- 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 SQKDLAGPTELLKTQVTKNKLGVLAPSQLQRYR------QELAERARLGYPSCFTNL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTFEFGEWCEFSPYEVGF--PKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLF-----EFNPFEMGSWDPTLNAFTDVKYLGTNVTNGK-----PVNKGQCIAGFDNTG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 YAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFIDLLTWR 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 WALINEAL-----YCALNTKGQSL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----YFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDV 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green NF2 protein - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: I54374
R;Pykett, M.J.; Murphy, M.; Harnish, P.R.; George, D.L.
Hum. Nol. Genet. 3, 559-564, 1994
A;Title: The neurofibromatosis Z (NF2) tumor suppressor gene encodes multipl
A;Reference number: I54374; MUID:94348500; PMID:8069298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GLLDCVSYITGASGSTWALANLYEDPEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 CSGGGYRAMLSGAGMLAAMDNRTDGANEHGLGGLLQGATYLAGLSGGNWLTSTLAMN-NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: :: | :: :: :: | :: :: | 1. :: :: | 1. :: :: | 1. :: :: | 1. :: :: | 1. :: :: | 1. :: :: | 1. :: :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: | 1. :: 
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                                                                                                                                                                                                                                                                                                                                                                                                            Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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A,Map position: 22q12.2-22q12.2
C,Superfamily: integrin beta chain; laminin-type EGF-like homology
                                                                                                                                                                                                                                                                                                                           Length 664;
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                                  A,Gene: SGD:PLB1
A;Cross-references: SGD:SO004610; MIPS:YMR008c
A;Map position: 131
C;Superfamily: yeast lysophospholipase
C;Keywords: transmembrane protein
F;648-664/Domain: transmembrane #status predicted <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 VRLGFGPCAEEQAFLSRR----KQVVAAALRQALQLDGDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 -IANLATDFLEDLSDNSDDIAIYAPNPFKEANFLQKNAT-
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Pred. No. 5.4e-06;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                       Query Match 5.0%; Score 162; DB 2; Best Local Similarity 21.5%; Pred. No. 0.00022; Matches 96; Conservative 64; Mismatches 170
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A;Molecule type: mRNA
A;Residues: 1-39 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 GEDNQNIPLVPLLQKERELDVIFALD 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 4.9%;
1 Similarity 79.5%;
31; Conservative
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R; Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, March 1995

A; Reference number: S53028

A; Accession: S53037

A; Molecule type: DNA

A; Molecule type: DNA

A; Cossidues: 1-664 < DEV

A; Cross-references: EMBL: Z48613; NID: 9728645; PIDN: CAA88523.1; PID: 9728655; MIPS: YMR0086
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RyArakawa, H.; Hayashi, N.; Nagase, H.; Ogawa, M.; Nakamura, Y.
RyArakawa, H.; Hayashi, N.; Nagase, H.; Ogawa, M.; Nakamura, Y.
RyArakawa, H.; Hayashi, N.; Nagase, H.; Ogawa, M.; Nakamura, Y.
RyArakawa, H.; Hayashi, N.; Nagase, H.; Ogawa, M.; Nakamura, Y.
RyArakawa, H.; Hayashi, N.; Nagase, H.; Ogawa, M.; Nakamura, Y.
RyArakawa, H.; Hayashi, N.; Nagase, H.; Ogawa, M.; Nakamura, Y.
RySeference number: 154375; MUD:94348501; PMD:8069299
RyScatus: preliminary; translated from GB/EMBL/DDBJ
RyScatus: preliminary; translated from GB/EMBL/DDBJ
RyScatus: preliminary;
RyScatus: Preferences: GB:S73853; NID:9688372; PIDN:AAB31736.1; PID:9688373
CyGenetics:
RyGenetics:
RyGenetics:
RyGenetics:
RyGenetics:
RyGenetics:
CySuperfamily: integrin beta chain; laminin-type EGF-like homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SSPYAAQKLLDVVDG 390
                                                                                                                                                                                                                                                   337 SNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLL 396
                                                                                                                                                             272 EFNPW-EFGTFD---PTIFGFVPLEYLGSKFEGGS----LPSNESCIRGFDSAGFVIGTS 323
WGRALSYQMFNASNGGLSYTWSSIADTPE-FQDGDYPMPFVVADGRNPGELVIGSNSTVY 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999
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R, Lee, K.S.; Patton, J.L.; Fido, M.; Hines, L.K.; Kohlwein, S.D.; Paltauf, J. Biol. Chem. 269, 19725-19730, 1994
A;Title: The Saccharomyces cerevisiae PLB1 gene encodes a protein required A;Reference number: A53647; MUID:94327513; PMID:8051052
                                                                                                                                                                                                                                                                                                                                                                                                                     397 TWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLC--LLDV---
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A;Cross-references: GB:L23089; NID:9437731; PIDN:AAA61611.1; PID:9437732
A;Note: the authors translated the codon GAC for residue 494 as Glu
                                                                                                                                                                                                                                                                                                                                    324 SSLFNQFLL-QINTISLPSFIKDVFNGILFDLDKSQNDIASYDPNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                     EFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRIC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 FEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLB1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YM8270.10c; protein YMR008c
C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.3%; Score 170; DB 2; Best Local Similarity 76.7%; Pred. No. 1.2e-06; Matches 33; Conservative 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 GEDGQ--NVPLHPLIQPERHVDVIFAVD 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----FYK-YNEH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GYLINTSCLPLLQPTRDVDLILSLD
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238
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                                                                                   Ribyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
Submitted to the EMBL Data Library, March 1999
A;Reference number: Z21962
A;Residues: L-623 < LINN>
A;Residues: 1-623 < LINN>
A;Residues: 1-623 < LINN>
A;Residues: Sirain 972h-; cosmid c1450
                                probable lysophospholipase precursor - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable lysophospholipase precursor - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 AGLKEL-----GLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 NAFDARNGNITSLGGILQSSMYLTGLSGGSWLVGSV----AVNNFANIT-FLHDDVWN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 WCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRIC-----FLEGIWSNLY 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -IEFGTWDTGVE---SFIPMEYTGTHLING----IPLNESCVRNFDNAGFLMGTSSNVF 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 FNNAVLSFLEMLAEDQLDVGLYPNPYQGYGNASN----TTTTNPLEPYPIIELIDGGSDS 425
                                                                                                                                                                                                                                                                                                                                                                                                                                             99 EQAFLSRRKQVVAAAL-----RQALQLD--GDLQEDEIPVVAIMATGGGIRAMTSLYGQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 TFSSVINETWEQD------GEFPFPIIIADNVIBGETVIPINDIVEFTP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 AANLODSLYWASEPSOFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWRP 400
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                                                  Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNT-KGQSL----TTFEFGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PATNASLTASNNT----
                                                                                                                                                                                                                                                                                                                                                                                                              Indels 147;
                                                                                                                                                                                                                                                                                                                                                                             Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 NKLGVLAPSQ------LQRYRQELAERARLGYPSCFTNLW------
                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.9%; Score 159.5; DB 2; Best Local Similarity 21.3%; Pred. No. 0.00032; Matches 96; Conservative 58; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455 INTSCLPLLOPTRDVDLILSLDYNLHGAFQ 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGIPFWPLLHPQRDVDVIFAID----GGYQ 451
                                                                                                                                                                                                                                                                                                             Map position: 3
Superfamily: yeast lysophospholipase
                                                                                                                                                                                                                                                                                              A; Gene: SPDB:SPCC1450.09c
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R;Churcher, C.M.
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A;Reference number: 221761
A;Accession: T38006
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-624 <CHU>A;Residues: 1-624 <CHU>A;Cross-references: EMBL: 299258; PIDN:CAB16353.1; GSPDB:GN00066; SPDB:SPACIA6.03c

submitted to the EMBL Data Library, September 1997

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95 PCAEEQAFLSRRKOVVAAALROALQ---LDGD----LQEDEIPVVAIMATGGGIRAMTSL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 ----EQSFIDKRIPKINTQMRSFISNTGLDVDVNSVINDSDGPRLGLAFSGGGLRAMVHG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 NVWNLEHSVFAPHGDNVVENLAYYDDLDDEIDQKKDAGFDTSLTDLWGRALSRKLVDATQ 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 EWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRIC-----FLEGIWSNL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TW-----DNGIK---AFLPMEYVGT-----HLKNGVPPDHKCIRNYDNAGFVMGTSATL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FNTFL---LEWSQEVTS-----NSTLYD----IIHKVFE-----KLSEDQNDI---A 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LVDGGEDDENIP 399
                                                                                                                                                                                                                                                                                                                                                                    36 PFFFFFEMESLSVAQAGVQWRD-LGSLQPPPLGFKRFSCLSLPSSWDYRLRELAVRLGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 GGVLNAFDSRNGNGSSLAGILQSAMYIAGLSGGSWLVGSV-----AVNNFANIT-YLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ALINEALLH--DEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 GGPNITFSSIRNOTWFONADYPYPIIISDSR---LEEEKAIP----ANTSIFEFTPYEFG
                                                                                                                                                                                                                                                                                                                                                                                                                     9 PLSLMQKREALAIS---LSKRDSVGSYAP----YNVTC---PS--DYMLRPASDGISSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 YAANLODSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLTWR
                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                    Query Match
4.9%; Score 159; DB 2; Length 624;
Best Local Similarity 22.5%; Pred. No. 0.00035;
Matches 112; Conservative 69; Mismatches 171; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYPNPYQNFTTTNTTVKNPFE-----RFDTID----
A;Experimental source: strain 972h-; cosmid clA6 C;Genetics:
A;Gene: SPDB:SPACIA6.03C
A;Map position: 1
C;Superfamily: yeast lysophospholipase
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Job time : 44.14 secs
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OM protein - protein search, using sw model

October 5, 2004, 19:13:29 ; Search time 24.2 Seconds (without alignments) 1301.754 Million cell updates/sec Run on:

US-09-830-321A-2 3235 1 MIFVELSPTLALCLERVASH........EQLLEALRQAVQRRRQRRPH 605 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			P47712 homo sanie	3 equips	mus mi		rattus	brachyd	P39195 homo sapien	homo	homo	homo	homo	homo	schiz			torn	P39457 penicillium		candida		neurospo	O59863 kluyveromyc			O13857 schizosacch	Q9uvx1 candida alb	P78854 schizosacch	_		schiz		_	
SUMMARIES		di	N	PA24 HORSE	PA24 MOUSE	PA24 CHICK	PA24 RAT	PA24 BRARE	ALU8 HUMAN	ALU2 HUMAN	ALU7 HUMAN					PLB3_YEAST	ALU1_HUMAN	PLB1_TORDE	PLB1 PENCH	PLB1_CANGA	PLB2 CANAL	PLB1_CANAL	PLB_NEUCR	PLB_KLULA	PLB1_YEAST		PLB2_SCHPO	PLB3_CANAL	PLB1_SCHPO	PLB2_CANGA	ALU4 HUMAN	PLB6 SCHPO	PLB2 YEAST	$\overline{}$	VGF_BPPHK
		BB		Н	Н	Н	-	Н	Н	Н	Н		Н	-	Н	-	Н	Н	Н	Н	Н	Н	м ,	-	Н,	٠,	٠,	н.	-	-	1	Н	Н	-	н
		Length	749	749	748	748	752	741	591	587	593	587	593	585	673	989	591	649	612	629	608	605	626	640	664	653	624	754	613	695	603	644	206	536	431
de	ery	Match	19.1	18.9	18.5	18.4	œ.	7.		6.2	•	•	٠	•			٠	•		5.3			٠,٠ ١,٠	•	•		٠	٠	٠	•	•	4.3	4.2	•	
		Score	619			S.	The second	572	226.5	199.5	199.5	٦,	192.5	191	186	184	182	177.5	177	172.5	165.5	164	164	o١	٥	ر ر د	nι	154 174	ς,	٠,	43	4	co.	\sim	0
	Result	No.	1	N	m	4	ഹ	9	7	20 1	ָּס יָ	10	11	12	£ 1.	14	15	16	17	18	19	20	221	7 (2.43	17	0 0	9 10	7 0	870	62	30	31	3.5	33

pg7738 rattus	P98171 homo sanien	O8w3k0 arabidonsis	P5540 rhizobium s	O9Dlt8 chlamvdia m	Ogrwh3 deinococous	091155 cricetulus	P30427 rattus norv	O69014 manchester	043556 homo sanien	P25059 hovine lenk	Q9y468 homo sapien
NPX2 RAT	RHG4 HUMAN	RDL3 ARATH	Y4FB_RHISN	EX5B_CHLMU	VATI_DEIRA	PLE1 CRIGR	PLE1_RAT	POLN MANCV	SGCE_HUMAN	POL BLVAU	LMBT_HUMAN
٦	Н	Н	н	Н	Н	-4	Н	Н	Н	_	Н
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43	946	1138	664	1026	69	4473	4687	2208	438	852	772
	3.1 946	F-1				۷.	٧.				
3.2		3.1	3.1	3.1	3.1	3.1	3.1	3.0	3.0	3.0	3.0

ALIGNMENTS

RESULT 1 PA24 HUMAN LD PA24 HUMAN LD PA24 HUMAN DT 01-FB DT 01-FB DT 10-OC DE CYtOS DE CYCOS DE CYCOS DE CYCOS DE CYCOS OC MAMME COC MAMME COC MAMME COC MAMME COC MAMME COC MAMME COC MAMME RR RR CLELL RR COLL RR MUTAGE RR MEDLIN RR MUTAGE RR MEDLIN RR MUTAGE RR MEDLIN RR A TABLEIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00168; C2; 1.
Pfam; PF00168; C2; 1.
SMART; SM00239; C2; 1.
SMART; SM00022; PLAO, 1.
PROSITE; PS50004; C2 DOWAIN 2; 1.
PROSITE; PS50004; C2 DOWAIN 2; 1.
Hydrolase; Lipid degradation; Calcium; Phosphorylation; 3D-structure.
DOMAIN 1 178 PROSPHOLIPID BINDING (PROBABLE).
                                                                                                                                                                                                                                                                 cytosolic phospholipase A(2), induces apoptosis, and potentiates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane vesicles in a calcium-dependent fashion.
TISSUE SPECIFICITY: Expressed in various tissues such as macrophages, platelets, neutrophils, fibroblasts and lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005829; C:cytosol; NAS.
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004623; P:phospholipase A2 activity; NAS.
GO; GO:0006690; P:elcosanoid metabolism; NAS.
GO; GO:0006663; P:platelet activating factor biosynthesis; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                              acylglycerophosphocholine + a fatty acid anion.
CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)0 = glycerophosphocholine + a fatty acid anion.
ENZYME REGULATION: Stimulated by agonists such as ATP, BGF, thrombin and bradykinin as well as by cytosolic Ca(2+).
SUBMINT: Interacts with HTATIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: The N-terminal C2 domain, by its association with membranes, mediates the regulation of CPLA2 by presenting active site to its substrate in response to elevations of
                                                                X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 16-141.
MEDLINE=98104145; PubMed=9430701;
Perisic O., Fong S., Lynch D.E., Bycroft M., Williams R.L.;
"Crystal structure of a calcium-phospholipid binding domain
                                                                                                                                                                                                                     MEDLINE=98332749; PubMed=9665851;
Xu G.-Y., McDonagh T., Yu H.-A., Nalefski E.A., Clark J.D.,
Cumming D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PīM: Activated by phosphorylation on a serine residue
                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 C2 domain.
                   prostaglandin production.";
Mol. Cell. Biol. 21:4470-4481(2001)
                                                                                                                                            cytosolic phospholipase A2.";
J. Biol. Chem. 273:1596-1604(1998)
                                                                                                                                                                                                  STRUCTURE BY NMR OF 1-138.
MEDLINE=98332749; PubMed=9665851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR00008; C2.
InterPro; IPR008973; C2 CalB.
InterPro; IPR002642; PLAc.
                                                                                                                                                                                                                                                                                                                                                                                       the inflammatory response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M72393; AAB00789.1; -. EMBL; M68874; AAA60105.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL022147; CAB42689.1;
PIR; A39329; A39329.
PDB; IRLW; 25-FEB-98.
PDB; IBCI; 13-JAN-99.
PDB; ICJY; 20-APR-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:9035; PLA2G4A.
MIM; 600522; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytosolic Ca(2+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelium.
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619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDYFQHP--HFSTWKATTLDGL-----PNQ-----LTPSEPHLCLLDVGYLINTSCL 460
                                                                                                                                                                                  154
                                                                                                                                                                                                                                                                                                                                                                         273 ALNIKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL 332
                                                                                                                                                                                                                                                                                                                                                                                         -------LLTWRPLAQATHNFLRGLHFH 415
                                                                                                                                                                                                            QAFLSRRKQVVAAALRQAL---QLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKE 156
                                                                                                                                                                                                                                                                  LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAPSQ 213
                                                                                                                                                                                                                                                                                215 SGILDCATYVAGLSGSTWYMSTLYSHPDFPEK---GPEBINEELMKNVSHNPLALLTPQK 271
                                                                                                                                                                                                                                                                                                                                      272 VKRYVESLWKKKSSGQPVTFTDIFGMLIGETLIHNRMNT-TLSSLKEKVNTAQCPLPLFT 330
                                                                                                                                                                                                                                                                                                                                                                                                                               EGIWSNLYA------ANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLL 376
                                                                                                                                                          66
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15-0TU-1999 (Rel. 38, Last sequence update)
15-UTU-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cycsolic phospholipase A2 (CPLA2) [Includes: Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase PLA24A OR PLA264 OR CPLA2.
Equus caballus (Horse)
                                                                                                                                                                                                                            LORYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDOREALSHGONPLPIYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                500 TSYPLSPLSDFATQDSFDDDELDAAVADPDEFERIYEPLDVKSKKIHVVDSGLTFNLPYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 PLLOPTRDVDLILSLDYNLHGA----FQQLQLLGRFCQEQGIPFPPISPSFEQLQPRE
                                                                                                                                                        BSLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRELA----VRLGFGPCAEE
                                                                                                                                                                                ETLGTATFTVSSMKVGEKKEVPFIFNQVTEMVLEMS----LEVCSCPDLRFSMALCDQE
                                                                                                                                 Gaps
                       BOTH PHOSPHOLIPASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                               174; Conservative 125; Mismatches 238; Indels 106;
                                                 S->A: DECREASES AGONIST-STIMULATED RELEASE OF ARACHIDONIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             721
           (BY MAPK)
                                     LYSOPHOSPHATASE ACTIVITY.
                                                                              9F9CDC5A98231C70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STENFOYPNQAFKRLHDLMHFNTLNNIDVIKEAMVESIEYRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559 HYTKVTYSQEDVDKLIHLTHYNVCNNQEQLLEALRQAVQRRRQ
                                                                                                       19.1%; Score 619; DB 1; 27.1%; Pred. No. 4.4e-40;
C2 DOMAIN.
PHOSPHORYLATION
S->A: ABOLISHES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 KIEEPPSTAGRIA--EFFTD---
                                                                              85210 MW;
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 106
505
228
                                                     505
                                                                               749 AA;
                                                                                                                       Similarity
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[1]
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228
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                                                                                 SEQUENCE
                                                                                                            Query Match
 DOMAIN
MOD_RES
                                                                                                                        Local
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                                                      MUTAGEN
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us-09-830-321a-2.rsp

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KRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLL----376
                           |: |: | | |: | | 379 KKYBENPLHFLMGVWGSAFSILFNRVLGVSGS---
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(Rel. 33, Last seg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLA2G4A OR PLA2G4 OR CPLA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytosolic phospholipase A2 (EC 3.1.1.4) (Phosphatidylc (EC 3.1.1.5)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 65:1043-1051(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PA24 MOUSE
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PA24 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 SHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLM 321
                                                     Claesson H.-E.;
"Purification, characterization and cDNA sequencing of calcium—
"Purification, characterization and cDNA sequencing of calcium—
"Purification, characterization and from equine neutrophils.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Selectively hydrolyzes arachidonyl phospholipids in the sn-2 position releasing arachidonic acid. Together with its lysophospholipid activity, it is implicated in the initiation of the inflammatory response.
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 VRLGFGPCAEEQAFLSRRKOVVAAALRQAL---QLDGDLQEDEIPVVAIMATGGGIRAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 SLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 GFSGVMKALYESGILDCATYLAGLSGSSWYMSTLYSHPDFPEK---GPEEINKELMKAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               vesicles in a calcium-dependent fashion (By similarity).
DOMAIN: The N-terminal C2 domain, by its association with lipid membranes, mediates the regulation of CPLA2 by presenting the active site to its substrate in response to elevations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Neutrophils;
Larsson Forsell P.K.A., Lindberg A., Karlsson S., Lindgren J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane
                                                                                                                                                                                                                                                                    acylglycerophosphocholine + a fatty acid anion.
CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)0 = glycerophosphocholine + a fatty acid anion.
ENZYME REGULATION: Stimulated by agonists such as ATP, EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95;
                                                                                                                                                                                                                                                                                                                                                                           thrombin and bradykinin as well as by cytosolic Ca(2+) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytosolic Ca(2+) (By similarity). PTM: Activated by phosphorylation on a serine residue (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.9%; Score 611.5; DB 1; Length 749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165; Conservative 121; Mismatches 212; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY MAPK)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 C2 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                749 AA;
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Best Local (
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-----QNKGSTMEEELENITAKHI 429
                                                    -AQAT 405
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REGURENCE FROM S. Feingold E.A. Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haigh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haigh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haigh F.,

RA Speleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Scheutz J., Myers R.M.,

R Hodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

R Hutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Human and mouse comb sequences.",

R Proc. Natl. Ard. Sci. U.S. A 99-1640-1640-1700-1
                                                                                        430 VSNDSSDSDDESQEPKGTENEDAERDYQNDNQASWVHRMLMALVSDSALFNTREGRAGKV 489
                                                                                                                                                                                                                                                                                                                                  506 SPEEQLQPRECHTFSDPTCP----GAPAVLHF-----SSGV-RRTPEEAAAGEV
                                                                                                                                                                                                                                                                   HNFLRGLHFHKDYFQHP--HFSTWKATTLDGL-----PNQ-----LTPSEPHLCLLD
                                                                                                                                                                                       490 HNFMLGLNLNTSYPLSPLRNFTTQESLDDDELDAAVADPDEFERIYEPLDVKSKKIHVVD
                                                                                                                                                                                                                                       VGYLINTSCLPLLQPTRDVDLILSLDYNLHGA-----FQQLQLLGRFCQEQGIPFPPISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 33, Last sequence update)
(Rel. 42, Last annotation update)
sspholipase A2
(Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark J.D., Lin L.-L., Kriz R.W., Ramesha C.S., Sultzman L.A.,
Lin A.Y., Milona N., Knopf J.L.,
"A novel arachidonic acid-selective cytosolic PLA2 contains a Ca(2+)-
dependent translocation domain with homology to PKC and GAP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-1- FUNCTION: Selectively hydrolyzes arachidonyl phospholipids in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     669 DIFDDPESPFSTFNFQYPNQAFKRLHDLMHFNTLNNIDVIKNAMVESIEYRRQ 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                             550 NL-SSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ
                                             -----KIEEPPSTAGRIAE--FFTD-LLTW--RPL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 MCVWGSAFSILFNRVLGVSGSQNKGSTMEEELENITAKHIVSNDSSDSDDBAQGPKGTEN 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLHVK-PDVSELMFADWVEFSPYEIGMAKYGTFWAPDLFGSKFFWGTVVKKYEENPLHFL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGIWSNLYA------ANLQDSL-----YWASEPSQFWDRWVRNQANLDK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETLGTATFPVSSMKVGEKKEVPFIFNQVTEMILEMS----LEVCSCPDLRFSMALCDQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 QAFLSRRKQVVAAALRQAL---QLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSBLFGSEFFMGQLMKRLPESRICFL
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                                                                                                                                                  thrombin and bradykinin as well as by cytosolic Ca(2+). SUBCELLUIAR LOCATION: Cytoplasmic. Translocates to membrane vesicles in a calcium-dependent fashion. DOWAIN: The N-terminal C2 domain, by its association with lipid anembranes, mediates the regulation of CPLA2 by presenting the active site to its substrate in response to elevations of cytosolic Ca(2+) (89 similarity).
sn-2 position releasing arachidonic acid. Together with its lysophospholipid activity, it is implicated in the initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99;
                                                                        acylglycerophosphocholine + a fatty acid anion.
CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)0 = glycerophosphocholine + a fatty acid anion.
ENZYME REGULATION: Stimulated by agonists such as ATP, EGF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 748;
                                                                                                                                                                                                                                                                                   PIM: Activated by phosphorylation on a serine residue (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                         the inflammatory response. CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)0 = 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00168; C2; 1.
Pfam; PF01735; PLA2_B; 1.
SMART; SM00239; C2; 1.
SMART; SM00022; PLAC; 1.
PROSITE; PS0004; C2 DOMAIN 2; 1.
Hydrolase; Lipid degradation; Calcium; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2 DOMAIN.
PHOSPHORYLATION (BY MAPK)
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49D12BBB2911492A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.5%; Score 599.5; DB 1;
llarity 26.9%; Pred. No. 1.4e-38;
Conservative 126; Mismatches 242;
                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 C2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     748 AA; 85222 MW;
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InterPro; IPR000008; C2.
InterPro; IPR009973; C2.Calb.
InterPro; IPR002642; PLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M72394; AAB00796.1; -. EMBL; BC003816; AAH03816.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
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Best Local Similarity
Matches 172; Conserv
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The phospholipase A2, a regulatory Ca(2+)-dependent lipid-binding domain a ca(2+)-independent catalytic domain.";

Thospholipase A2, a regulatory Ca(2+)-dependent lipid-binding domain a ca(2+)-independent catalytic domain.";

The lol (1 Chem. 26):18249 (1994).

The lol (2 Chem. 26):18249 (1994).

The position releasing arachidomic acid. Together with its sn-2 position releasing arachidomic acid. Together with its sn-2 position releasing arachidomic acid. Together with its implicated in the initiation of the inflammatory response.

Tysophospholipid activity, it is implicated in the initiation of the inflammatory response.

The inflammatory response.

The inflammatory response.

CHALITIC ACTIVITY: Phosphatidylcholine + H(2)O = acylalycerophosphocholine + a fatty acid anion.

CHALITIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O = glycerophosphocholine + a fatty acid anion.

CHALITIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O = glycerophosphocholine + a fatty acid anion.

CHALITIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O = glycerophosphocholine + a fatty acid anion.

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CHALITIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O = glycerophosphocholine + a fatty acid anion.

CHALITIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O = glycerophosphocholine + a fatty acid anion.

CHALITIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O = glycerophosphocholine + a fatty acid anion.

CHALITIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O = glycerophosphatidylcholine + a fatty acid anion.

CHALITIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O = glycerophosphatidylcholine + a fatty acid anion.

CHALITIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O = glycerophosphatidylcholine + a fatty acid anion.

CHALITIC ACTIVITY: 2-lysophosphatidylcholine + 
                                                    507
                                                                                                         464
                                                                                                                                                        RDFS----SQDSFDDELDAAVADPDEFERIYEPLDVKSKKIHVVDSGLTFNLPYPLILR 562
                                                                                                                                                                                                               519
                                                                                                                                                                                                                                                                                                                        SDPTCP----GAPAVLHF-----SSGV-RRTPEEAAAGEVNL-SSSDSPYHYTK 562
                                                                                                                                                                                                                                                                                                                                                               623 K-PKNPDVEKDCPTIIHFVLANINFRKYKAPGVLRETKEEKEIADFDIFDDPESPFSTFN 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytosolic phospholipase A2 (CPLA2) [Includes: Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
                                            450 BEAE--KEYQSDNQASWVHRMLMALVSDSALFNTREGRAGKVHNFMLGLNLNTSYPLSPL
                                                                                                           ----HLCLLDVGYLINTSCLPLLQ
                                                                                                                                                                                                                  PTRDVDLILSLDYNLHGA----FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTF
                                                                                                                                                                                                                                                                 PORGVDLIISFDFSARPSDTSPPFKELLLAEKWAKMNKLPFPKIDPYVFDREGLKECYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
AQATHNFLRGLHFHKDYFOHP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94299545; PubMed-8027085;
Nalefski B.A., Sultzman L.A., Martin D.M., Kriz R.W., Towler P.S.,
Knopf J.L., Clark J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: Activated by phosphorylation on a serine residue (By
                                                                                                                                                                                                                                                                                                                                                                                                                                 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : | | : : | | | : : | | | 682 FQYPNQAFKRLHDLMYFNTLNNIDVIKDAIVESIEYRRQ 720
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        EQVPLLKIEEPPSTAGRIAEFFTDLLTWRPL
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SIMILARITY: Contains 1 C2 domain.
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                                                                                                              -HFSTWKATTLDGLPNQLTPS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
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[2]
ERRATUM.
                                                                                        Rattus
                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                     44 ESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRELAVRLGFGPCAEEQAFL 103
                                                                                                                                                                                                                                                                                                                                         160
                                                                                                                                                                                                                                                                                                                                                                 218
                                                                                                                                                                                                                                                                                                             100 ETLGMATFPISSLKLGEKKEVQLTFNNVTEMTLELSLEV-CSSTDLRFSMALCDEEKKFR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                   RQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIW 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381
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                                                                                                                                                                                                                                                                                                                                                   || :|| ||||| :: || |:: :| DCATYIAGLSGSTWYMSTLYSHDDFPEK---GPKEINQELMNSVSHNPLLLLTPQKVKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 PSTAGRIA-----EFFTDLL------TWRPLAQATHNFLRGLHFHKDYFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            505 SPLADLLTQESVEEDELDAAVADPDEFERIYEPLDVKSKKIHIVDSGLTFNLPYPLILRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 SRRKQVVAAALRQALQLDGD---LQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLL
                                                                                                                                                                                                                                                                                                                                                                                     DCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAPSQLQRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 GSAFSILFNRVLGVSNS------QNKGPTMEBELENIRLKHLVSNDSSDSEDESQHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          466 TRDVDLILSLDYNLHGA-----FQQLQLLGRFCQEQGIPFPPISPSPEEQLQPRECHTF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SDPTCPGAPAVLHF-----SSGV-RRTPEEAAAGEVNL-SSSDSPYHYT
                                                                                                                                                                                                                                                             Matches 166; Conservative 129; Mismatches 245; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HP--HFSTWKATTLDGL-----PNQ-----LIPSEPHLCLLDVGYLINTSCLPLLQP
                            Length 748;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          682 NFQYPNEAFKRLHDLMEFNTLNNLDVIKQAMMESIEYRKE
                                                                                                                                                                                                                                        18.4%; Score 596; DB 1; 25.9%; Pred. No. 2.7e-38;
or send an email to license@isb-sib.ch)
                      EMBL; U10329; AAA53228.1;
                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   218
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752 AA

STANDARD;

PA24 RAT P50393;

DA DA

RESULT 5

PA24_RAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-203 (Rel. 41, Last annotation update)
Cytosolic phospholipase A2 (CPLA2) [Includes: Phospholipase A2
(EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with lipid
nting the
                                                                                                                                                                             Owada Y., Tominaga T., Yoshimoto T., Kondo H.; "Molecular cloning of rat cDNA for cytosolic phospholipase A2 and tincreased gene expression in the dentate gyrus following transient forebrain ischemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membranes, mediates the regulation of CPLA2 by presenting active site to the substrate in response to elevations of cytosolic Ca(2+) (By similarity) PTM: Activated by phosphorylation on a serine residue (By
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Pancreatic islets;
                                                                                                                                                                                                                                 Brain Res. Mol. Brain Res. 25:364-368(1994)
                                                                                                                                                                                                                                                                               Owada Y., Tominaga T., Yoshimoto T., Kondo
Brain Res. Mol. Brain Res. 27:355-355(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity). SIMILARITY: Contains 1 C2 domain.
                                                                                                                                                                                                                                                                   MEDLINE=95206125; PubMed=7898324;
                                                                                                                                                                                                                                                                                                                                               MEDLINE=98223459; PubMed=9555100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calb.
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                                                                           PLA2G4A OR PLA2G4 OR CPLA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR008973; C2 Ca
InterPro, IPR002642; PL\overline{
m A}C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P47/12; 122.
InterPro; IPR00008; C2.
TDR008973; C2_
                                                                                           (Rat)
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                           norvegicus
                                                                                                                            NCBI_TaxID=10116;
                                                  (ĒC 3.1.1.4) (
(EC 3.1.1.5)].
                                                                                                                                                                   TISSUE=Brain;
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01-0CT-1996 (Rel.
                    15-MAR-2004
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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTFRRQFKENIKENMKKLLGPKKSEGLYSTRDVPVVAILGSGGGFRAMVGFSGVMKALYE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LORYROELAERARLGYPSCFINLWA-LINEALLHDEPHDHKLSDOREALSHGONPLPIYC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALNIKGQSLITFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 RDFSPQDSFDDDELDAAVADPDEFERIYEPLDVKSKKIHVVDSGLTFNLPYPLILRPQRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SSGV-RRTPEEAAGEVNL-SSSDSPYHYTKVTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 MGVWGSAFSILFNRVLGVSGSQNKGSTMEEELENITAKHIVSNDSSDSDDEAQGPKGTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BDAE--REYONDNOASWVHRMLMALVSDSALFNTREGRAGKEHNFMLGLNLNTSYPLSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDLILSLDYNLHGA-----FQQLQLLGRFCQEQGIPFPISPSPEEQLQPRECHTFSDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAPSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQVPLLKIEEPPSTAGRIAEFFTDLLTWRPL-----AQATHNFLRGLHFHKDYFQHP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAFLSRRKQVVAAALRQAL---QLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKE
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                                                              ; 1.
Calcium, Phosphorylation.
PHOSPHOLIPID BINDING (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                    Length 752;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                      C2 DOMAIN.
PHOSPHORYLATION (BY MAPK)
SIMILARITY).
                                                                                                                                                                                                                                                                                                                -> T (IN REF. 3).
C68F71BB05FBF732 CRC64;
                                                                                                                                                                                        C - S (IN REF. 3).

R -> O (IN REF. 3).

Q -> I (IN REF. 3).

MST -> IVP (IN REF. 3).

S -> I (IN REF. 3).

E -> V (IN REF. 3).

P -> T (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                      249;
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                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.4%; Score 594; DB 1;
Best Local Similarity 26.9%; Pred. No. 3.8e-38;
Matches 171; Conservative 125; Mismatches 249
                                                                                                                                                                                                                                                                                                                                85706 MW;
                                                                              PROSITE; PS50004; C2 DOMAIN 2;
Hydrolase; Lipid degradation;
    Pfam; PF00168; C2; 1.
Pfam; PF01735; PLA2_B; 1.
SMART; SM00239; C2; 1.
SMART; SM0022; PLAC; 1.
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                                                                                                                                                                                                                                                                        410
489
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505
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159
287
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752 AA;
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                          DOMAIN
MOD_RES
                                                                                                                                                                                              CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Manufekti B.A., Sultzman D.A., Martin D.M., Kriz R.W., Towler P.S., Knopf J.L., Clark J.D.;
Knopf J.L., Clark J.D.;
Poblination of two functionally distinct domains of cytosolic phospholipase A2, a regulatory Ca(2+)-dependent lipid-binding domain and a Ca(2+)-independent catalytic domain.";
J. Biol. Chem. 269:18239-18249(1994).
-: Function: Selectively hydrolyzes arachidonyl phospholipids in the sn.2 position releasing arachidonic acid. Together with its lysophospholipid activity, it is implicated in the initiation of the inflammatory response.
-: CATALYTIC ACTIVITY: Phosphaidylcholine + H(2)0 = 1-
acylglycerophosphocholine + a fatty acid anion.
-: CATALYTIC ACTIVITY: 2-lysophosphaidylcholine + H(2)0 =
                                                                          (BC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase); Lysophospholipase (BC 3.1.1.5)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycerophosphocholine + a fatty acid anion.
ENZYME REGULATION: Stimulated by agonists such as ATP, EGF, thrombin and bradykinin as well as by cytosolic (a(2+).
SUBCELLULAR LOCATION: Cytoplasmic. Translocates to membrane vesicles in a calcium-dependent fashion (By similarity).
DOMAIN: The N-terminal C2 domain, by its association with lipid amenbranes, mediates the regulation of CPLA2 by presenting the active site to its substrate in response to elevations of cytosolic Ca(2+) (By similarity).
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                          Phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Activated by phosphorylation on a serine residue (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 1; Length 741;
1.9e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115; Mismatches 236; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZFIN; ZUB-GRAGE________
InterPro; IPRO00099 C2.
InterPro; IPRO008973; C2 CaLB.
InterPro; IPRO02642; PLĀC.
PĒan; PF001735; PLA2_B; 1.
PMART; SM00239; C2; 1.
SMART; SM00022; PLAc; 1.
PROSITE; PS50004; C2_DOWAIN_2; 1.
PROSITE; PS50004; C2_DOWAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34896B1A8364A9D4 CRC64;
                                                             [Includes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION
34, Last sequence update)
43, Last annotation update)
                                                                                                                                                    PLA2G4A OR PLA2G4 OR CPLA2.
Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.7%; Score 572;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 C2 domain.
                                                                (CPLA2)
                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Embryo;
MEDLINE=94299545; PubMed=8027085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, B54908; B54908.
HSSP, P47712; 1BCI.
ZFIN; ZDB-GENE-990415-45; cpla2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           741 AA; 83809 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase, Lipid degradation;
DOMAIN 1 172 P
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Best Local Similarity 26.5'
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7955;
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89 VRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDG----DLQEDEIPVVAIMATGGGIRAM 144

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741 AA

PRT;

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PA24_BRARE ID PA24_BRARE AC P50392; DT 01-OCT-1996 01-0CT-1996

(Rel. 34, Created)

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202 TKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREA 260
                                                                                              SNNPLKLILPQNINRYVKALMKKKSAGQPVTFTDIFGMLIGETLIPGR-MNIKLSSLKGK 313
                                                                                                                                    432
                                                                                                                                                                                                            366 ANLDK---EQVPLLKIEEPPSTAGRIAEFFTDLL-----TWRPLAQATHNFLRGLHFH 415
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                                      201
                                                      198 VGFSGVMKALYESGVFDCATYVAĞLSGSTWYMSMLYSHPEFPAK---GPGDINKELMNRV 254
                                                                                                                      LSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQL 320
                                                                                                                                                                                                                                                                                                                                                              613 VFKPAKGDKNC---PTIIHFVLANINFRNFKAPGVPRDSDKDIEFGDFDIFDEPASPYST 669
                                                                                                                                                                     ---AANLQDSLYWASEPSQFWDRWVRNQ 365
                                                                                                                                                                                                                                                        416 KDYFQHPHFSTWKATTLDGLPNQLT-PSE------PHLCLLDVGYLINTSCLPL 462
                                                                                                                                                                                                                                                                                                                            612
                                145 TSLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQV
                                                                                                                                                                                433 EETQRGGTESADAEDERQRHAQASWVQRMLTSIMGDTTLFTTREGRAGKVHNFMLGLNLN
                                                                                                                                                                                                                                                                                                                493 STLPFSPFSGITHQISLBEEVDAVTDPDEFERIYEPLDVKSKKIHVVDSGLIFNLPYPLI
                                                                                                                                                                                                                                                                                                   LQPTRDVDLILSLDYNLHGA----FQQLQLLGRFCQEQGIPFPPISPSEEQLQPRECH
                                                                                                                                                                                                                                                                                                                                              518 TF----SDPTCPGAPAVLHF-----SSGV-RRTPEEAAAGEVNL-SSSDSPYHY
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"Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences.";
Genomics 12:838-841(1992).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
                                                                                                                                                                                                                                                                                                                                                                                                        670 FNFKYNNQAFKRLHDLMEFNTLINNIEVIKEAIKDSILLRRE 710
                                                                                                                                                                                                                                                                                                                                                                                        561 TKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ 601
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Homo sapiens (Human)
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01-FEB-1995 (Rel. 31, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       591 AA
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Quentin Y.;
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                                                                                                                                                                    MKRLPESRICFLEGIWSNLY--
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Claverie J.-M., Makalowski W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 371:752-752(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                          "Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANGOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS PALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA libraries also contain partial and/or rearranged CDNAs ligated with Alu-derived sequence in any orientation. Although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons, consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with
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CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5 or 3 'untranslated regions. However, CDNA libraries also contain partial and/or rearranged cDNAs.
                                                                                                                                                                                                                                                                                                             CODON, YXXX IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
-!- CAUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 PAPCPFFFFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRE----
                                                                                                                                                                                                                                                                                                                                                                                                       acid sequences. CAUTION: Alu repetitive sequences are interspersed in human and
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Alu subfamily SB sequence contamination warning entry.
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01-FEB-1995 (Rel. 31, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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FRAME-3.
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FRAME-5.
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                          MEDLINE=91178815; Pubmed=1706781; Jurka J., Milosavljevic A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coding nucleotide sequence.
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ALU FAMILIES CLASSIFICATION
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DOMAIN

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sapiens (Human)
                   REPEATS.
      CONCEPT
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JUNEA J., Milosavijevic A.;
"Reconstruction and analysis of human Alu genes.";
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANBOUS: VARIOUS ANALYSES (SER REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
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FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claverie J.-M.; "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria, Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                    "Alu alert.";
Nature 371:752-752(1994)
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                           NCBI_TaxiD=9606;
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primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5' or 3' untranslated regions. However, CDNA libraries also contain partial and/or rearranged cDNAs ligated with Alu-derived sequence in any orientarion. Although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with
MISCELLANBOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. COUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino acid sequences.
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FRAME-2. FRAME-3. FRAME-4. FRAME-1.

194 292 391

100 198 296

DOMAIN

DOMAIN

EMBL; U14568; -; NOT ANNOTATED CDS.

Hypothetical protein. DOMAIN

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493 FFETESRSVAQAGVQWRDLGSLQAPPPGFTPFSCLSLPSSWDYRRPPPRPANFCIFSRDG 552
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CAUTION: Alu repetitive sequences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5' or 3' untranslated regions. However, cDNA libraries also contain partial and/or rearranged cDNAs ligated with Alu-derived sequence in any orientation. Although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. CAUTION: This Alu entry is provided in order to avoid the further
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALU FAMILIES CLASSIFICATION.
MEDLINE=91178815; PubMed=1706781;
Jurka J., Milosavljevic A.;
Weconstruction and analyse of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-! MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The Alu family developed through successive waves of fixation closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).
                                                                 Length 587;
                                                                                                    Indels
                                                                                                                                    40 FFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRE
                                                                                                                                                                                                                                                                                                                                                                                                                      Alu subfamily SQ sequence contamination warning entry.
                              3EAAB3E3E3929203 CRC64;
                                                                                                    14;
                                                                 DB 1;
                                                             Score 199.5; DB 1
Pred. No. 1.1e-07;
1; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 31, Last sequence update) (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                593 AA.
              FRAME-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95021758; PubMed=7935834;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claverie J.-M., Makalowski W.;
"Alu alert.":
                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                  63703 MW;
                                                                     6.28;
                                                                                   65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALU FAMILIES CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Alu alert.";
Nature 371:752-752(1994).
                                                                                                     42; Conservative
                                                                                                                                                                                                                                                                                                                                  STANDARD;
489
587
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                  587 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                     Similarity
                                                                                                                                                                                                                                              553 VSPC 556
                                                                                                                                                                                                           93 FGPC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claverie J.-M.;
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                                                                                                                                                                                                                                                                                                                                  ALU7 HUMAN
                                SEQUENCE
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 FFLRRSFALVAQAGVQWRDLGSLQPPPPGFKRFSCLSLPSSWDYRRPPPRPANFCIFSRD 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 FFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRE-----LAVRL 91
consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with
                                                                                                   putative protein sequence
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                                                                              being reported.
CAUTION: Any significant similarity of a putative protein seque with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the
                                                               the consequence of erroneous Alu-derived amino acid sequences
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-FEB-1995 (Rel. 31, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
Alu subfamily SB1 sequence contamination warning entry.
Homo sapiens (Human).
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54A4F50F33A6089F CRC64;
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                                                                                                                                                                                                                                     modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 199.5; I Fred. No. 1.1e-1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587 AA.
                                                                                                                                                                                                                                                       entities requires a license agreement (or send an email to license@isb-sib.ch)
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FRAME-2.
FRAME-3.
FRAME-4.
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MEDLINE-88333009; PubMed=3138422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92241891; PubMed=1572661;
                                                                                                                                           coding nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                            64417 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claverie J.-M., Makalowski W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity 63.1%;
41; Conservative
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295
395
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Best Local 8
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0
                                                                                                                                                                                                                                                                                                                                                                                          CDNA libraries also contain partial and/or rearranged CDNAs ligated with Alu-derived sequence in any orientation. Although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons. consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with
                                                                                                                                               THAT ALU REPEATS FALL INTO 8 SUBFANTLIES. THEREFORE, 8 ALU WARNING CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the coding nucleotide sequence.
                                                                                                                                                                                                                                                                                                                      CAUTION: Alu repetitive sequences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5' or 3' untranslated regions. However,
                                                                                                                                                                                                                       MISCELLANBOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. CAUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino
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                                                                  Jurka J., Milosavljavic A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the consequence of erroneous Alu-derived amino acid sequences
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Homo sapiens (Human).
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01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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FRAME-2.
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FRAME-5.
FRAME-6.
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                                 ALU FAMILIES CLASSIFICATION.
MEDLINE=91178815; PubMed=1706781;
   J. Mol. Evol. 27:194-202(1988)
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296
395
493
587 AA;
                                                                                                                                                                                                                                                                                                    acid sequences
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P39193;
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1D ALUG HU

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OS HOME
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

64603 MW; 136EF344AACD12A2 CRC64;

593 AA;

SEQUENCE

S

us-09-830-321a-2.rsp

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SEQUENCE FROM N.A.
Mammalia; Euther
NCBL_TaxID=9606;
                                 REPEATS.
      "Alu alert.
         CONCEPT.
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196 295 395 494 593

101 200 299 399 498

DOMAIN DOMAIN DOMAIN

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PRT;
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MEDLINE=95021758; Pubmed=7935834;
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                                                                                                                                    40; Conservative
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Best Local Similarity
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ALUS_HUMAN
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"INDICATES THE PRESENCE OF A STOP

CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.

-!- CAUTION: This Alu entry is provided in order to avoid the further

pollution of protein sequence databases with Alu-derived amino

acid sequences.

-!- CAUTION: Alu repetitive sequences are interspersed in human and

primate genomes with an average spacing of 4 kb. Some of them are

contrively transcribed by pol III. Normal transcripts may contain

Alu-derived sequences in 5 or 3 untranslated regions. However,

CDNA libraries also contain partial and/or rearranged CDNAs

ligated with Alu-derived sequence in any orientation. Although Alu

claments (especially situated on the complementary strand) have a

great potential to create additional/alternative exons,

consideration should be given to the possibility that the presence

of an Alu in an open reading frame may have resulted from a

cloning artifact or may be due to misinterpretation of sequencing

data. This point has been overlooked on several occasions, with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JULKA O. MILLORAN 1974. ...
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANDOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
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CAUTION: Any significant similarity of a putative protein sequence
with an Alu-translated entry must be taken as a warning that a
part of Alu repeat may have been artifactually included in the
                                                                                                                                                                                                                                                                                                                                                                                                     Claverie J.-M.; "Identifying coding exons by similarity search: alu-derived and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the consequence of erroneous Alu-derived amino acid sequences
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                potentially misleading protein sequences.";
Genomics 12:838-841(1992),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAME-1.
FRAME-2.
FRAME-3.
FRAME-4.
FRAME-5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91178815; PubMed=1706781;
Jurka J., Milosavljevic A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88333009; PubMed=3138422; Quentin Y.;
                                                                                                                                               MEDLINE=95021758; PubMed=7935834;
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92241891; PubMed=1572661;
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                                                                                                                                                                                    Claverie J.-M., Makalowski W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALU FAMILIES CLASSIFICATION
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                                                                                                               299 FFLRRSFALVAQAĞVQMRDLGSPQPPPGFKRFSCLSLPSSWDYRHAPPRPANFCIFSRD 358
                                                                              91
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Jurka J., Milosavljevic A.;

Jurka J., Milosavljevic A.;

Jeconstruction and analysis of human Alu genes.";

J. Mol. Evol. 32:105-121(1991).

-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA libraries also contain partial and/or rearranged cDNAs ligated with Alu-derived sequence in any orientation. Although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons, consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid sequences.

CAUTION: Alu repetitive sequences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5' or 3' untranslated regions. However,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
                                                                              39 FFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRE-----LAVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to avoid the further
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. CAUTION: This Alu entry is provided in order to avoid the furthe pollution of protein sequence databases with Alu-derived amino
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The Alu family developed through successive waves of fixation closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).
                                      7;
Length 593;
                                        Indels
                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Alu subfamily SC sequence contamination warning entry.
Homo sapiens (Human).
6.0%; Score 192.5; DB 1;
61.5%; Pred. No. 3.8e-07;
trive 1; Mismatches 17;
                                                                                                                                                                                                                                                                                                            585 AA
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                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                               noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                                                         393 FFXDGVSL-CRQAGVQWRDLGSLQPPPPGFKRF8CLSLPSSWDYRRAPPRPANFCIFSRD 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490 XFFETESRSVARLEC-----SGALSAHCNLRLPGSSDSPASASRVAGTTGARHHAQLI 542
                                                                                                                                                                                                                                                                                                                                                                                    39 FFFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRE-----LAVRL 91
                                              CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the
cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFGPCABEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQL
                                                                                                                                                                                                                                                                                                                                                                70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 AGL----KELGLLDCVSYITGASGSTWALANL----YEDPEWSQKDLAGPTE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21048401; PubMed=11859360; Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Encoks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
           data. This point has been overgoned we consequence of erroneous Alu-derived amino acid sequences
                                                                                                                                                                                                                                                                                                                                        Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last amnotation update)
Putative lysophosholipase C977.09c precursor (EC 3.1.1.5)
(Phospholipase B)
SPAC977.09C OR SPAC1348.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 ---LLKT----QVTKNKLGVLAPSQLQRYRQELAERARLGYPSCF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 FVFLVETGPHHVGQDGLDLLT-----SXSARLGLPKCW 575
                                                                                                                                                                                                                                                                                                                                                               63; Indels
                                                                                                                                                                                                                                                                                                               46EE8C4F493650A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                    5.9%; Score 191; DB 1; 31.7%; Pred. No. 4.9e-07;
                                                                                                                                                                                                                                                                                                                                                              20; Mismatches
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                                                                                                                                                                      entities requires a license agreement (St
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                          EMBL; U14571; -; NOT_ANNOTATED_CDS. Hypothetical protein.
                                                                                    coding nucleotide sequence.
                                                                                                                                                                                                                                                                                                              63957 MW;
                                                                                                                                                                                                                                                                                                                                                    31.7%;
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                                                                                                                                                                                                                                      95
193
291
389
487
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393
491
585 AA;
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Q9P327;
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Advances K., Jones L., Jones M., Leather S., McDonald S., McLean J., Money P., Woule S., Mungall K., Murphy L., Niblett D., Odell C., A. Diver K., O'Neil S., Pearson D., Quail M., Rabbinowitsch E., Rutherford K., Rutter S., Sanders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Radylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Radylor K., Taylor R., Roben J., Grymonprez B., Reiger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rabert E., Denzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Goffeau A., Cadieu E., Dreano S., Cloux S., Lelaure V., Mottier S., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Jucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Sanchez M., del Rey F., Benito J., Sanchez M., del Rey F., Porsburg G., Porser M., del Rey F., Porsburg M., del Rey F., Porsburg M., del Rey F., Porsburg M., del Rey F., Hermanner M., del Rey F., Hermanner M., del Rey F., del M., del Rey M., del Rey F., del M., del Rey M., del Rey F., del M., del Rey M., de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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N-LINKED (GLCNAC. . ) (POTENTIAL).

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11.1%; Pred. No. 1.5e-06;
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InterPro, IPR001179, FKBP_PPIase.
InterPro, IPR002642, PLAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL358912; CAB94277.1; -. EMBL; AL137130; CAB69631.1; -.
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Best Local Similarity 21.1*
Matches 148; Consorvative
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEP--PSTAGRIA-- 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LHGAFQQLQLL 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----EFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSE 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TT-----SIVDSD 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 MONDDSIWDLSDSIVTPGGINIFKTAKRWDHISNAVESKONADYNTSLADIWGRA-LAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 ESAWLEKRNKVTSVALKDFLTRATANFSDSSEVLSKLFNDGNSENLPKIAVAVSGGGKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --YEDPEWSOKD---LAGPTELLKTOVTKNKL-GVLAPSOLORYROELAE---RARLGYP
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Pred. No. 2.1e-06;
); Mismatches 192; Indels 214;
                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 SCFTNLWALINE-----ALLHDEPHDHKLSDQREALSHGQNPLPIYCA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 MTSLYGQLAGLKEL-----GLLDCVSYITGASGSTWALANL---
                 PIR, S66693, S66693.

Germonline; 144433; -.
SGD; 8006371; PLB3. -.
SGD; 80005371; PLB3. -.
GO; GO:0006615; C:extracellular space; IDA.
GO; GO:0004622; F:lysophospholipase activity; IMP.
GO; GO:0006660; P:phosphoinositide metabolism; IDA.
GO; GO:0006660; P:phosphoinositide metabolism; IDA.
InterPro; IPR002642; PLAC.
Pfam; PF01735; PLA2 B; 1.
SMART; SM00022; PLAC.
I.ipid degradatio; Advirolase; Glycoprotein; Signal.
ILipid degradatio; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRFCQEQGIPFPPISPSPEEQLQPRECHTF-----SDPTCPGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95A2DBF41BF3E20F CRC64;
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                                                                                                                                                                                                                                                                      POTENTIAL.

INSOPHOSPHOLIPASE 3
POLY-SER.

N-LINKED (GLCNAC.)

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75076 MW;
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Best Local Similarity 21.0
Matches 129; Conservative
EMBL; Z74753; CAA99010.1;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

coding nucleotide sequence.

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ALC FAMILIES CLASSIFICATION.

MEDLIES-9170815; PubMed=1706781;

Jurka J., Milosavijevic A.;

"Reconstruction and analysis of human Alu genes.";

J. MOL. Evol. 32:105-121(1991).

-! MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE

THAT ALU REPRATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING

CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX

FRAMES. CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                 Claverie J.-M.;
"Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences.";
Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANBOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. CAUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino
                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The Alu family developed through successive waves of fixation closely connected with primate lineage history.", J. Mol. Evol. 27:194-202(1988).
                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alu subfamily J sequence contamination warning entry.
                                                                                                                                             591 AA
                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                 MEDLINE=95021758; PubMed=7935834;.
Claverie J.-M., Makalowski W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALU FAMILIES CLASSIFICATION.
MEDLINE-88333009; PubMed=3138422;
Quentin Y.;
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92241891; PubMed=1572661;
                                           588 LLEALRQAVQRRRQR 602
                                                           554 FMGCVGCAIIRRKQQ 568
                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                         Nature 371:752-752(1994)
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                           ALU1 HUMAN
P39188;
                                                                                                                                                                                                                                                                                                                                              "Alu alert
                                                                                                                                                                                                                                                                                                                                                                                       CONCEPT.
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HUMAN
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CAUTION: All repetitive sequences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5' or 3' untranslated regions. However, CDNA libraries also contain partial and/or rearranged CDNA ligated with Alu-derived sequence in any orientation. Although Aluellents and the state of the complementation is although Aluellents.

acid sequences.

great potential to create additional alternative exons, consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may been to misinterpretation of sequencing data. This point has been overlooked on several occasions, with the consequence of erroneous Alu-derived amino acid sequences

CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the

being reported.

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                                                                                                                                                                                          Gaps
                                                                                                                                                                                         .,
                                                                                                                                                                       Length 591;
                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                      40 FFEMESLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR 83
                                                                                                                                                      665D395735519D95 CRC64;
                                                                                                                                                                      Query Match 5.6%; Score 182; DB 1;
Best Local Similarity 81.8%; Pred. No. 2.5e-06;
Matches 36; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                  5, 2004, 19:25:33
                                                                                                    FRAME-1.
FRAME-2.
FRAME-3.
                                                                                                                           FRAME-4
                                                                                                                                     FRAME-5
                                                                                                                                              FRAME-6
                                                                                 EMBL; U14567; -; NOT_ANNOTATED_CDS. Hypothetical protein.

DOMAIN

1 96 FRAME-
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393
492
591
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Job time: 27.2 secs
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298
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496
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RESULT 1
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0860v8 mus musculu
086vy8 homo sapten
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080vv9 mus musculu
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075457 homo sapien
Q8n176 homo sapien
Q7tn01 mus musculu
Q9p8ll cryptococcu
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Q9dbx5 mus musculu
                                                                                                                            5, 2004, 18:51:24; Search time 120.193 Seconds (without alignments) 1588.179 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9ukv7 homo sapien
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                                                                                                                                                                                                                                                        1 MIFVELSPTLALCLERVASH......BQLLEALRQAVQRRRQRRPH 605
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                     1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
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O95712
Q80VV8
Q86XP0
Q8IUP3
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Q7TN01
Q9P8L1
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Q9DBX5
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Gapop 10.0 , Gapext 0.5
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sp_rodent:*
sp_virus:*
sp_vortebrate:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
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sp_mhc:*
sp_organelle:*
sp_organelle:*
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Maximum DB seq length: 200000000
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3235
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ALIGNMENTS

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9

Gaps

459 123 519 183

83

243

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LLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYG 303
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                                                                                                                                                                            TGLLVLFCPAPCPFFFFFFFFFFFSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR
                                                                                                                                                                                                       TGTFRFHCPA-C----WEQE-LSI-----RLODAPEEQLKAPLSALPSGOVVR
                                                                                                                                                                                                                                       ------LRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQLDGD
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                     49;
                                                                                                                        DB 4; Length 1012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
, group IVB (Cytosolic) (Fragment)
                                                                                                                                                   Indels
                                                                                               CRC64;
           85.5%; Score 2767.5; DB 4;
87.6%; Pred. No. 6.4e-231;
live 5; Mismatches 22;
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STRAIN-FVB/N; TISSUE-Salivary gland;
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01-JUN-2003 (TrEMBLrel. 24, Las
01-JUN-2003 (TrEMBLrel. 24, Las
01-OCT-2003 (TrEMBLrel. 25, Las
Similar to phospholipase A2, gr
Mus musculus (Mouse)
InterPro; IPR003347; TF_JmjC.
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                                                           ---LRELAVRIGEGPCAEEQAFLSRRKQVVAAALRQALQLDGD
                                                                                 LVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKGVVAAALRQALQLDGD
                                                                                                                                 EWSOKDLAGPTELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEA
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 TGLIVLFCPAPCPFFFFFFFFFFFSCLSVAQAGVQWRDLGSLQPPPLGFKRFSCLSLPSSWDYR
                               ------RLQDAPEEQLKAPLSALPSGQVVR
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytosolic phospholipase A2 beta.
CPLA2 BETA.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99185108; PubMed=10085124;
Pickard R.T., Strifler B.A., Kramer R.M., Sharp J.D.;
"Molecular cloning of two new human paralogs of 85-kba cytosolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew, HGNC:9036; PLA2G4B.
Genew, HGNC:9036; PLA2G4B.
GO, GO:0004627; F:calcium-dependent cytosolic phospholipase A.
InterPro; IPR000008; C2.
InterPro; IPR008973; C2 CallB.
InterPro; IPR002642; PLÃc.
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J. Biol. Chem. 274:8823-8831(1999).
-- SIMILARITY: CONTAINS 1 C2 DOMAIN.
EMBL, AF065215; AAC78836.1; --
                       1000 RQAVQRRRQRRPH 1012
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                                   TGTFRFHCPA-C-
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                         46.1%; Score 1492; DB 4; Length 8 51.6%; Pred. No. 2.6e-120; rive 92; Mismatches 152; Indels
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC035335; AAH35335.1; -.
GO; GO:0004620; F:phospholipase activity; IEA.
GO; GO:000595; P:phospholipid catabolism; IEA.
InterPro; IPR000008; C2.
InterPro; IPR008973; C2.Calb.
              Pfam; PF01735; PLA2_B; 1.
SMART; SM00239; C2; 1.
SMART; SM00022; PLAC; 1.
PROSITE; PS50004; C2 DOWAIN 2; 1.
SEQUENCE 818 AA; $\overline{9}1955 N\overline{W}$; E5ADF3478FDAB1B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches 296; Conservative
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                                                                                                                                                           Query Match
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                DB 11; Length 439;
                                                                                                                                                                                                                                                      Query Match
59.7%; Score 1931.5; DB 11; Lengt
Best Local Similarity 82.5%; Pred. No. 6.9e-159;
Matches 358; Conservative 30; Mismatches 35; Indels
                               the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Imai Y., Chiba H.;
"cytosolic phospholipase A2 homolog(cPLA2delta).";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB090876; BAC67158.1;
GO; GO:0004620; F:phospholipase activity; IEA.
GO; GO:0003395; P:phospholipid catabolism; IEA.
                                                                                                                                                                                                           439 AA; 50464 MW; EA9041FA820F5F10 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Cytosolic phospholipase A2 delta.
CPLA2 DELTA.
Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ dat EMBL; BC042758; AAH42758.1; -. PIR; PT0721; PT0721. PT0721. GO: GO:0004620; F:phospholipiase activity; IEA. GO: GO:0009395; P:phospholipid catabolism; IEA. InterPro; IPR02642; PLAC. PLAC. Pfam; PF01735; PLA2_B; 1. NON TER SEQUENCE 439 AA; S0464 MW; EA9041FA820F5F10 C.
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InterPro; IPR00893; C2 CalB.
InterPro; IPR002642; PLAc.
Pfam; PP00168; C2, 1.
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421 EAMHQAVQRRRKRK 434
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                                                                                                                                       2 IFVELSPTLALC------LERVASHLTDTGLLVLFCPAPCPFFFFFEMESLSVAQAGVQ
                                                                                                                                                                                  WRDLGSLQPPPLGFKRFSCLSLPSSWDYRLRELAVRLGFGPCAEEQAFLSRRKQVVAAAL
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                                                                                                                    Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                    55;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to phospholipase A2, group IVB (Cytosolic) (Fragment).
                                                                                            35.3%; Score 1141.5; DB 4; Length 845; 41.1%; Pred. No. 7.4e-90; ive 95; Mismatches 220; Indels 55;
                                                                         845 AA; 93280 MW; 32FEBBB34FF96D53 CRC64;
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SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Salivary gland;
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last and
                                                     PROSITE; PS50004; C2_DOMAIN_2; 1. NON TER 1 1 SEQUENCE 845 AA; 93280 MW; 32
                                                                                                          al Similarity 41.1%;
258; Conservative 9
  InterPro; IPR002642; PLAC.
Pfam; PF00168; C2; 1.
Ffam; PF01735; PLAC_B; 1.
SMART; SM00239; C2; 1.
SMART; SM00022; PLAC; 1.
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Matches 258
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Q80VV9;
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ESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTA 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLYGQLAGLKELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTELLKTQVTKNK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPLPIYCALNIKGQSLITFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 TRLETPMSSFSQAVLDIFTSRITCAQTFNFTRĞLCMYKDYTARKDFVVSEDAMHSHNYGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 -DGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGVLAPSQLQRYRQELAERARLGYPSCFTNLWALINEALLHDEPHDHKLSDQREALSHGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 ELAVRIGEGPCAEEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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01-MRR-2003 (TYEMBLrel. 23, Last sequence update)
01-MRA-2003 (TYEMBLrel. 23, Last sequence update)
01-UNA-2003 (TYEMBLrel. 24, Last annotation update)
11-UNA-2003 (TYEMBLrel. 24, Last annotation update)
Hypothetical lysophospholipase catalytic domain containing
protein.

Bus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                              Length
EMBL, BC039947; AAH39947. L; -. EMBL/GenBank/DDBJ databases. EMBL, BC039947; AAH39947. L; -. GO; GO:0004620; F:phospholipase activity; IEA. GO; GO:0009395; P:phospholipid catabolism; IEA. InterPro; IPR000008; C2. InterPro; IPR008973; C2.Cal.B. InterPro; IPR008973; C2.Cal.B. InterPro; IPR008973; C2.Cal.B. Pfam; PF00169. C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FCOEQGIPFPPISPSPEEQLOPRECHTFSDPTCPGAPAVLHF---
                                                                                                                                                                                                                                                                                                                                               841 AA; 95063 MW; D03F239BECA2BBE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         atch

24.8%; Score 1127; DB 11;

231 Similarity 42.6%; Pred. No. 1.3e-88;

231; Conservative 100; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą.
                                                                                                                                                                                                    PEGM; PF00168; C2; 1.
Pfam; PF00168; C2; 1.
Pfam; PF001735; PLA2_B; 1.
SMART; SM0023; C2; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
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261 LSHGQNPLPIYCALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQL 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00168; C2; 1,
Pfam; PF0135; PLA2_B; 1.
SMART; SM00239; C2; 1,
PROSITE; PS50004; C2 DOMAIN_2; 1.
PROSITE; PS00136; SUBILIASE_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000008; C2.
InterPro; IPR0008973; C2 Calb.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR002642; PLAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595 AVQRRRQ 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 ALDRRRQ 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 SCLS-----LPSSWDYRLR------BLAVRLGFGPCAEEQAFLSRRKQVVAAALRQA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 ALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCALNTKGQSLTTPEFGEWCEFSPYEV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CSTBL/64; TISSUE=Cerebellum;

MEDLINE=22254683; PubMed=12466851;
The FANTOM CONSORTIUM;
The FANTOM CONSORTIUM;
The RANGOM CONSORTIUM;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
To '770 full-length cDNAS.";
The Malysis of the mouse transcriptome based on functional annotation of 6,770 full-length cDNAS.";
The Malysis of the mouse transcriptome based on functional annotation of 6,770 full-length cDNAS.";
The Mature 420:563-573 (2002).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 LQLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKELGLLDCVSYITGASGSTWALA
                                                                                                                                                                                                                                                                                                                                                                                                                         26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWAS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q80VQ8;

Q80VQ8;

Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)

Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)

Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Similar to phospholipase A2 (Fragment).

Similar to phospholipase A2 (Fragment).

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                            21.9%; Score 70%; DB 11; Length 356; 49.2%; Pred. No. 8.6e-53; Live 43; Mismatches 81; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%; Score 685; DB 11; Length 372; 39.5%; Pred. No. 9.1e-51; .ive 68; Mismatches 126; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R., Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 AA; 42638 MW; 17BD15B59207ABBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMEM.; BC046400; ANA46400.1; GO; GO:0004620; F:phospholipase activity; IEA. GO; GO:0009395; P:phospholipid catabolism; IEA InterPro; IPR005642; PIAC. PEAC. PEAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=NMRI; TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 49.23
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 145; Conserva
                                     SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
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321 MKRLPESRICFLEGIWSNLYAANLODSLYWASEPSQFWDRWYRNQANLDKEQVPLLKIEE 380
                                                                                                         881 PPSTAGRI-----AEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHF----STWKA 429
                                                                                                                                                                                                                                                                                               430 TTL---DGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQL 486
                                                                                                                                                                                                                         179 HNYGYPDACPNQLTPMKDFLSLVDGGFAINSPFPLVLQPQRAVDLIVSFDYSLEGPFEVL 238
                                                                                                                                                                                                                                                                                                                                                                                                                  QLLGRFCQEQGIPFPPISPSPEEQLQPRECHTFSDPTCPGAPAVLHF-----SS 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 GV-RRIPEBAAAGEVNLSSSDSPYHYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQ 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
09TT38;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phosphatidyl choline 2-acylhydrolase cPLA2.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N [1]

P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

Al-Khalili O.K., Eaton D.C.;

Al-Khalili O.K., Eaton D.C.;

"Molecular cloning of cDNA coding for phospholipase A2.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

C -!- SIMILARITY: CONTRINE C 22 DOMAIN.

EMBL; AF204923; AAF15299.1; -.

R HSSP; P47712; IBCI.

R GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0004289; F:subtilase activity; IEA.

R O; GO:0004289; F:subtilase activity; IEA.

R O; GO:0004508; F:phospholipae activity; IEA.

R O; GO:0006508; P:proteolygis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          748 AA; 85235 MW; 7661A3EFC41FF668 CRC64;
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97

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558
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                                                                                                                                                                                             YCALNIKGQSLITFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFWGQLMKRLPESRIC 330
                                                                                                                                                                                                                                                376
                                                                                                                                                                                                                                                                          438
                                                                                                                                                                                                                                                                                                    414
                                                                                                                                                                                                                                                                                                                                                      HKDY-----FQHPHFSTWKATTLDGLPNQ-----LTPSEPHLCLLDVGYLINTSCL 460
                                                                                                                   269
 : | |
-----LRFSMALCD 152
                                       154
                                                                                                                                                                                                                                                                                                                                                                            499 NTSYPLSPLRDFTQESFDDDELDAAVADPDEFERIYEPLDVKSKKIHVVDSGLTFNLPYP
                                                                                                                                                                                                                                                                                                                                                                                                                        CHTFSDPTCP----GAPAVLHF-----SSGV-RRTPEEAAAGEVNL-SSSDSPY
                                                                                                                                                                   QKVKRYVESLWKKKSSGQPVTFTDIFGMLIGETLIHNRMHT-TLSSLKEKVSSAQCPLPL
                                                                                                                                            SQLQRYRQELAERARLGYPSCFINLWA-LINEALLHDEPHDHKLSDQREALSHGONPLPI
                                                                                                                                                                                                             FLMGVWGSAFSILFNRVLGVSGS------HNKGSTMEEBLENITAKHIVSNDSSDSD
                                                                                                                                                                                                                                                                                                    ---AQATHNFLRGLHF
                                                                                                                                                                                                                                                                                                                           439 DESQEPKGTEGEDAEREYONDHQASWVHRMLMALVSDSALFNTREGRAGKVHNFMLGLNL
                                                                                                                                                                                                                                                                                                                                                                                                          461 PLLOPTRDVDLILSLDYNLHGA----FOOLOLLGRFCQEQGIPFPPISPSEEQLOPRE
                                      EEQAFLSRRKQVVAAALRQAL---QLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGL
                                                       155 KELGLLDCVSYITGASGSTWALANLYEDPEWSQKDLAGPTEL---LKTQVTKNKLGVLAP
                                                                                                        213 YESGILDCATYIAGLSGSTWYMSTLYSHPDFPEK---GPQEINBELMKNVSHNPLLLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buka<u>r</u>yota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W. Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                  FLEGIWSNLYAANLQDSLYWASEPSOFWDRWVRNQANLDKEQVPLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STFNFQYPWQAFKRLHDLMYFNTLNNIDVIKDAWVESIBYRRQ 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601
HYTKVTYSQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                       -KIEEPPSTAGRIA--EFFTD-LLTW--RPL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22341132; PubMed=12454917;
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genetic and genomic tools
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dyn. 225:384-391(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
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SEQUENCE 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    559
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.E., Scheetz T.E.,
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Jones S.J., Marra M.A.;
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCOS6041; AAHS6041.1; -.
Hypothetical protein.
SEQUENCE 749 AA; 85282 MW; CE769904144C4DE2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             219;
                                                                                                                                                                                                                                                                                                                                                                                                                              19.2%; Score 622; DB 13; 27.6%; Pred. No. 7.9e-45;
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214 LORYROELAERARLGYPSCFINLWA-LINEALLHDEPHDHKLSDOREALSHGONPLPIYC 272
                                                                                  207 SGILDCATYIAGLSGSTWYMSTLYSHPDFPEK---GPEEINEELMKNVSHNPLLLLTPQK 263
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Pickard R.T., Strifler B.A., Kramer R.M., Sharp J.D.;
"Molecular cloning of two new human paralogs of 85-kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60948 MW; 63E6AEE7F7550741 CRC64;
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Last annotation update)
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J. Biol. Chem. 274:8823-8831(1999).
EMBL; AF065214; AAC78835.1; -.
PIR; T13162; T13162.
GO; GO:0004620; F:phospholipase activity; IEA.
GO; GO:003395; P:phospholipid catabolism; IEA.
InterPro; IRRO2642; PLAC.
Pfam; PF01735; PLA2.B; 1.
SMART; SM00022; PLAC; 1.
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RX MEDLINE-2108566; PubMed=11217851;
RX Arakwa T., Shinaqa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakwa T., Shinagawa A., Shibata K., Komoo H., Adachi J., Fukuda S.,
Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Matsuda H.A., Ashburnar M., Batalov S., Yamanaka I.,
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RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bolunga N., Carninci P., de Bonado M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Lyonone P., Marchhonni L., Mashima J., Mazaarelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
RA Gaski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Hayashizaki Y., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y., Tayo-oka K., Haseegawa Y., Kawaji H., Kohtsuki S.,
RT. "Functional annotation of a full-length mouse cDNA collection.";
RT. "Functional annotation of a full-length mouse conva
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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PROSITE; PS00136; SUBTILASE ASP; 1.
SEQUENCE 740 AA; 84268 MW; E2A1296AAF52937E CRC64;
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MGD: MGI:1195256; Pla2g4a.
GO:0004620; F:phospholipase activity; IEA.
GO: GO:0004289; F:subtlase activity; IEA.
GO: GO:000395; P:phospholipid catabolism; IEA.
GO: GO:000508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                             740 AA.
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-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
EMBL; AK004701; BAB23486.1; -.
                                                                                                                                             Created)
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000008; C2.
InterPro; IPR0000973; C2.Calb.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR002642; PLAc.
                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
Phospholipase A2, group IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00168; C2; 1.
Pfam; PF01735; PLA2_B; 1.
                                                                                       PRELIMINARY;
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SMART; SM00022; PLAC; 1.
                                                                                                                                                                                                                                                                       (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             PLA2G4A OR PLA2G4
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                  Mus musculus
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Best Local S
                                                                                     Q9DBX5
                                  RESULT 11
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273 ALNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRICFL 332
                                        -----ANLQDSL-----YWASEPSQFWDRWVRNQANLDK 370
                                                                                                                                                                                                                                                                            |: | : : | : | 442 BEAE--KEYQSDNQASWVHRMLMALVSDSALFNTREGRAGKVHNFMLGLNLNTSYPLSPL 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     615 K-PKNPDVEKDCPTIHFVLANINFRKYKAPGVLRETKEEKEIADFDIFDDFSSFSTFN 673
                                                                                                                                                                                                                                                                                                                                                            --EP-----HLCLLDVGYLINTSCLPLLQ 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 EEQAFLSRRKQVVAAALRQALQLDGDLQEDEIPVVAIMATGGGIRAMTSLYGQLAGLKEL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 GLLDCVSYITGASGSTWALANLYE---DPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                 465 PTRDVDLILSLDYNLHGA----FQQLQLLGRFCQEQGIPFPPISPSFEGLQPRECHTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SSGV-RRIPEEAAAGEVNL-SSSDSPYHYTK
                                                                                                                                                                                                                                       371 EQVPLLKIBBPPSTAGRIAEFFTDLLTWRPL-----AQATHNFLRGLHFHKDYFQHP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEKAAVERREHVLKALKKL----RIEADEAPVVAVLGSGGGLRAHIACLGVLSEMKEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota: Metazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytosolic
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15.4%; Score 498.5; DB 4; Length 541;
Best Local Similarity 27.8%; Pred. No. 2.5e-34;
Matches 158; Conservative 86; Mismatches 190; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
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317 MGQLMKRLPESRICFLEGIWSNLYAANLQDSLYWASEPSQFWDRWVRNQA-NLDKEQVPL 375
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                                                                                                                   117 AKSLOKTIQAARSENYS-LIDEWAYMVISKQIRELPESH-LSNMKKVVEEGILPYPIFAA 174
                                                                                                                                                                                                                                                                          -----LYA--ANLQDSLY 349
                                                                                                                                                                                                                                                                                                                  233 TFİRĞIMGSALGNTEVIREYIFDQLRNLTLKGLMRRAVANAKSIGHLIFARLLRİQESSQ 292
                                                                                                                                                                                                                                                                                                                                                                                               293 GEHPPPEDEGGEPEHTWLIEMLENWTR--TSLEKQEQP----HEDPERKGSLSNLMDFVK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TOLLITWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSEPHLCLLDV 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GPVVIHF------PLFNIDACGGDIBAWSDTYDTFKLAD 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 L-----KIEE---PPSTAGRIAEFFTDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WKATTLDGLPNOLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q----PRECHTFSDPTCPGAPAVLHFSSGVRRTP---EEAAAGEVNLSSSDSPYHYTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYLINTSCLPLLQPTRDVDLILSLDYNLHGAFQQLQLLGRFCQEQGIPFPPISPSEBQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLLDCVSYITGASGSTWALANLYE---DPEWSQKDLAGPTELLKTQVTKNKLGVLAPSQL
                                                                                         QRYRQELAERARLGYPSCFTNLWA-LINEALLHDEPHDHKLSDQREALSHGONPLPIYCA
                                                                                                                                                                                  ----LNTKGQSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRI
                                                                                                                                                                                                                                                                                                                                                                 W-----ASEPSQFW----DRWVRNOANLDKEQVPLLKIEEPPSTAGRIAEFF---
                                               -----LKHRFTROEW-----DL
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 3.6e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similar to phospholipase A2, group IVB (Cytosolic)
Homo sapiens (Human).
                              |||| |:|: | ||||||::||
|GLLDAVTYLAGVSGSTWAISSLYTNDGDMEALEAD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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39.5%;
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SEQUENCE 216 AA; 24371 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 DLWSKAPASCYILKGET
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                                                                                                                                                                                                                                                                                 CFLEGIWSN-----
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Strausberg R.;
Submitted (JUL-2002)
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nes 92; Conserv
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                                                                                                                                                                                                                                                                                        GEHPPPEDEGGEPEHTWLTEMLENWTR--TSLEKQEQP----HEDPERKGSLSNLMDFVK 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q-----PRECHTFSDPTCPGAPAVLHFSSGVRRTP---EEAAAGEVNLSSSDSPYHYTKV 563
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that is
                                                                                                                                                                                                   175 IDNDLQPSWQEARAPE--TWFEFTPHHAGFPALGAFVSITHFGSKFKKGRLVRTHPBRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W-----ASEPSOFW-----DRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFF----
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                                                                                                                                                                         ---LNTKGOSLTTFEFGEWCEFSPYEVGFPKYGAFIPSELFGSEFFMGQLMKRLPESRI
                                                                                                                                                                                                                                                                                                                                                                                                                                            -TDLLTWRPLAQATHNFLRGLHFHKDYFQHPHFSTWKATTLDGLPNQLTPSBPHLCLLDV
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C TISSUE=Skeletal muscle,
   TISSUE=Skeletal muscle,
   TISSUE=Skeletal muscle,
   TISSUE=Skeletal muscle,
   MEDILINE=98371032; PubMed=9705332;
   MEDILINE=98371032; PubMed=9705332;
   MEDILINE=98371032; PubMed=9705332;
   To reprylated and contains homology to cPLA2.";
   To reprylated and contains homology to cPLA2.";
   To hiol. Chem. 273:21226-21323 (1998).
   EMBL; AF058921; AAC32223.1; -.
   Genew; HGRC:9037; PLA2G4C.
   RO; GO:001628; PLA2G4C.
   RO; GO:001628; P.Calcium-independent cytosolic phospholipase...;
   InterPro; IPR002642; PLAC.
   RO; GO:00222; PLAC.
   RO; MART; SM00222; PLAC.

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.2%; Score 490.5; DB 4; Length larity 27.6%; Pred. No. 1.3e-33; Conservative 86; Mismatches 191; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60920 MW; BBB972A611FB5237 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08, Created)
08, Last sequence update)
24, Last annotation update)
                564 TYSQEDVDKLLHLTHYNVCNNQEQLLEAL 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 541
                                                                                                                                                                                                                                                                     330 CFLEGIWSN-
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nes 157; Conserv
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075457
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Ridusberg R.L., Septengold E.A., Grouse L.H., Schaefer C.F., Schuler G.D.,
A Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brapleton M.J., Solares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Robak S.A., McKwan D.N., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan K.J., Malek J.B., Mullahy S.J.,
Richards S., Morley K.C., Hale S. Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S. Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
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487 QLLGRFCQEQGIPFPPI-SPSPEEQLQPRECHTFSDPTCPGAPAVLHFSSGVR 538
                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Buks musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; 
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EMBL; BC054740; AAHS4740.1; -.
Hypothetical protein.
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202 EGPVTYSEAPRMNVDAMLLDLVMAYFTDMNDPSIKDKLCALQQALGTETDEFGIEMAEII 261
                                                                          262 ONWNETSAEKKEQFLDHLLDRFKKTQEDTTTYSLANWNTGLVWDRCVFVNETRKCVSKWQ 321
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                                                                                                                   429 ATTL-----DGLPNQLTPSEPHLCLLDVGYLINTSCLPLLQPTRDVDLILSLDYNLHG
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	S ⊞ S	Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; (Mammalia; Eutheria; B. I (bases 1 to 726) Liu, XQ., Zhou, Y.,	Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Liu,XQ., Zhou,Y., Zhang,LJ	nan) Da; C La; P 26)	Chordata; Craniata; Primates; Catarrhin. Zhang,LJ., Xu,H.,	·I	Vertebrata; Euteleostomi; ; Hominidae; Homo. Chen.HK Pan.ZG. and	ostomi; -G and
have a ng printed,	TITLE JOURNAL COMMENT	Zeng,YX. Transcription Unpublished (Contact: YiXi Cancer Center	Zeng, Y X. Transcriptional Gen Unpublished (2003) Contact: YiXin Zeng Cancer Center	Sene	Zeng,YX. Transcriptional Gene Expression Profile Unpublished (2003) Contact: YiXin Zeng		Human Nasopharynx	
iption 1191 EST8114 h 6812 603084703 7051 Homo sapi 7052 Pan trogl	FEATURES source	Sun rac- 651 Dong Tel: 86- Fax: 86- Email: y	1 acres University 651 DongFeng Road Bast, Guan Tel: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@gzsums.edu.cn Location/Oualifier: 1726 /organism="Homo sag /mol_type="mRNA"	East East -743 506 wms.e	f, GuangZhou adu.cn. Lifiers Dmo sapiens"	ou 510060, China		

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us-09-830-321a-4.rst

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/.clone_libe="Wild" MGC 120"
/clone_libe="Wild" MGC 120"
/note="Organ: pooled pancreas and spleen; Vector:
pcWv-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dr primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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                     can
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11563 row: e column: 01
High quality sequence start: 4
High quality sequence stop: 680.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 527.6; DB 12; Length 680;
Pred. No. 7.7e-119;
0; Mismatches 4; Indels 4;
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                                                                                                                                                                                                                                  /lab_host="DH10B"
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al Similarity 98.6%;
574; Conservative (
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/tolone_lib="human nasopharynx"
/note="isSTs generated from a normal nasopharynx cDNA
library from southern Chinese"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Pration: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                      ;
                                                                                                                                      Length 726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
1 (bases 1 to 680)
                                                                                                                                                                      Indels
                                                                                                                                        DB 14;
                                                                                                                                        Score 587.2; DB 14;
Pred. No. 1.8e-133;
0; Mismatches 3;
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI836812
BI836812.1 GI:15948362
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99.5%;
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Homo sapiens
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19; Conservative
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                                                                                                                                            Query Match
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Pan troglodytes PLA2G2D gene, VIRTUAL TRANSCRIPT, partial sequence, genenic survey sequence.
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Pan troglodytes
Pan troglodytes
Pan troglodytes
Pan troglodytes
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Pan troglodytes
Pan troglodytes
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 438)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenhaum,D.M., Civello,B.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Iu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 GGGATCCTGAACTAAGATGGTCAAGCAAGTGACTGGGAAAATGCCCATCCTCC
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Pred. No. 1.6e-96;
0; Mismatches 1; Indels 0;
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/locus_tag="HCM6095"
             421 CAGACCCCTGGGTGCTAG 438
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99.8%;
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                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 438)
Clark, G., Glannowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M. A., Tanembaum, D. M., Civello, D. R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X. H., White, T. J., Sninsky, J. J., Adams, M.D. and Cargill, M.
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   AY417051
Homo sapiens PLA2G2D gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA. This sequence was made by sequencing genomic exons and ordering them based on alignment.
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                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 438)
Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Direct Submission
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                                                                                                                                                                                                                                                                                                                Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="HCM6095"
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                                                                 AY417051.1 GI:39773011 GSS.
                                        genomic survey sequence
                                                                                                               Homo sapiens (human)
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1. .461
| organism="Sus scrofa"
| organism="Sus scrofa"
| wol_type="mRNA"
| db xref="taxon:9823"
| tissue_type="lymphoid"
| cell type="maroxphage"
| lab host="DH10B"
| lobe="lib="jns"
| note="Vector: pSPORTI; Site 1: NotI; Site 2: SalI;
| ibrary made from pools of polyA selected RNA. Macrophages
| were derived from peripheral blood monounclear cells
| cultured for 48 hrs on plastic in the presence of 30% L929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is Neilan, J.G., Kutish, G.F., Lu, Z., Zsak, A. and Rock, D.L. sequence analysis of African swine fever virus infected and non-infected porcine macrophage cDNA libraries non-infected porcine macrophage cDNA libraries on the contact: Neilan JG contact: Neilan JG contact: Neilan JG plum Island Animal Disease Center US Department of Agriculture, Agricultural Research Service DS Box 848, Greenport, NY 11944-848, USA Tel: 631 323 3044

Fax: 631 323 3044

Email: jneilan@pladc.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified by cross match v0.990329 and lucy v1.17p.
                                                                                                                                                                                                                                  TGACAAGGAGGTGGCCTTCTGCTGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCG 420
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
1 (bases 1 to 461)
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                                                         AGTGACTGGGAAAATGCCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG
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Pred. No. 1.2e-68;
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Sus scrofa
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                                                                                                                                                                                                 EST 30-NOV-2001
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         Unpublished (2001)
Contact: Dr. Judith F. Margolin
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@txcc.org
Seq primer: M13 primer.
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                             463 bp mRNA linear EST 30-NOV-20
TCBAP1Q13560 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1356, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 463)
Wei,Y., Tesng,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr.,
Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
Pediatric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCBAP1356"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                            CAGACCCCTGGGTGCTAG 466
                                                                                                                                                                                                                                                           sequence.
BM153087
BM153087.1 GI:17177919
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                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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Query Match Best Local S: Matches 429

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ACCESSION VERSION KEYWORDS SOURCE

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Mammala; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musculla (Dases I to 623)

Mammala; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. CE I (Labese I to 623)

Nikaido, I., Osato, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Kiyosami, T., Riyosawi, T., Tomaru, Y., Basegawa, Y., Mogami, J., Kiyosawi, T., Tomaru, Y., Basegawa, Y., Mogami, J., Kiyosawi, C., Copolori, T. Baldarelli, R., Hill, D.P., Bult, C., Hune, D.A., Quackenbush, J., Schrim, L.M., Kanapin, A., Matsuda, H., Reisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Pavan, W.J., Perta, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Sultana, R., Takenaka, Y., Taylor, M. Stecou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teagule, R.D., Tonita, M., Vang, I., Wang, I., Yang, L.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY752231 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830213F07 5', mRNA sequence.
                                                                                                       61 GATGGCTGGTGTGTGATTCCAATCCAGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
                                                                                                                                                                                                                                                                                                                                                                                                    296
                                       42 TCTGTCTCCACTGCTCTGTGCTGGGGATCATGGAACTTGCACGGCTGTGGGGCTGGTGGT 101
                                                                                                                                                                                                                                                                                                                                                     281
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                                                                                                                                                                                                                             181 TGGCAGAGGCC-AACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCT
                                                                                                                                                                                                                                                                                                                                      240 ATGACCACCTGAAGACCCAGGGGTGCGG-CATCTACAAGGA-CTATTACAGATA-CAACT
                                                                                                                                            102 GAIGGCIGGIGIGAIGCCGAICCAGGGGGGAICCIGAAGCIGAAGCIAGAIGGICAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                          342 TITCCCAGGGAACAICCACTGCTCTGACAAGGAAGCTGTGTGTGTGAGATGCTGTGT
              TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGGCTGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 GCCTGTGACAAGGAGGTGGCCTT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402 GCCTGTGACAAGGAGGTGGCCTT 424
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BY752231.1 GI:27183012
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BY752231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 AGTCACCTGAAGGGCCATGCCGCACCCACTTGGACCACTACAGATACACCTTTTCC 128
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                            CTGCCTCCACTGCTCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTG
                                                                         307 GTGACCGGGAAGGTGCCCTTCTTCTCCTATTGGCCCTACGCTGTCACTGTGGAATCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                          242 GACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCC
                                                                                                                                       62 ATGGCTGTGATTCCAATCCAGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAA
                                                                                                                                                                                                                                                                                                                               182 GGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 GACAAGGGGGTGGCTTTCTGCATGAAGCGGAACCTGGACAGCTACAAGAAGCACCTGCGT
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 424)
Liu.X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G.
Zeng,Y.-X.
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/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"
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Unpublished (2003)
Contact: YiXin Zeng
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       65; Indels
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651 DongFeng Road Bast, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
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96.3%; Pred. No. 3.9e-65;
live 0; Mismatches 9;
    Mismatches
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/db_xref="taxon:9606"
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    Conservative
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Best Local Similarity 96.3
Matches 369; Conservative
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TACTACT 1
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Matches 362;
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CD687559
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus adult male thymus CDNA, RIKEN full-length enriched library, clone:5830452G11 product:phospholipase A2, group IID, full insert sequence.
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366
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Analysis of the mouse transcriptome based on functional annotate of 60,770 full-length CDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1582)
6 (bases 1 to 1582)
7 (Carninol, P., Fukuda, S., Rukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatushi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatushi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatushi, Y., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
                                                                                                                                                                                                                                                                                            367 GACAAGGAGGTGGCCTTGTGCTTGAAGCANAACCTGGATAGCTACAATAAGCGCCTGCGT
                                                                                                                       362 GACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCGT
                                                                            CAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCAGCTGTGTGCCTGT
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Bnzymol. 303, 19-44 (1999)
10349636
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust (Medical Genetics Hospital Cambridge) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246
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                                                                                                                                                                                                                                                                                                       Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Tuctani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Saski,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission.
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/clone_lib="RIKEN full-length enriched, activated spleen"
                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computational Analysis of Full-Length Mouse cDNAs Compared with
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
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llarity 77.5%; Pred. No. 4.3e-62;
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/mol_type="mRNA"
/strain="NOD"
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                                                                 Contact: Yoshihide Hayashizaki
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GSS 17-DEC-2003
                   361
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                                                                                                                                                                                                                                                                                 367 GACAAGGAGGTGGCCTTGTGCTTGAAGCAAAACCTGGATAGCTACAATAAGCGCCTGCGT 426
                                                                                                                                                                                                                                                                                                                                                                  427 TACTACTGGCGGCCCCGTTGCAAAGGCAAGACTCCAGCATGCTAAAGGGAGTCCACTCTGT 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 438)
Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 GGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAAATGCCCATCCTCTC 148
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438 bp DNA linear GSS 17-DEC-2
                                                                              GACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCC
                                                                                                                                                                                                                                                                                                                          422 ITCTACTGGCGGCCCCACTGCCGGGGGCAGACCCCTGGGTGGTAGAAGCCCACACCCTCT
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                                                                                                                                                               CAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGT
                                                                                                                                                                                                                                             362 GACAAGGAGGIGGCCTTCTGCCTGAAGGGCAACCTGGACTACCAGAAGGGACTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 AIGGAACTIGCACTGCTGTGGGGCTGGTGATGGCTGGTGTGATTCCAATCCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAGACTCGCCTGCTGTGTGGGCTGCTGGCCGGTGGTATAACTGCAACCCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 289.8; DB 2
Pred. No. 1.7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="PLA2G2D"
/locus_tag="HCM6095"
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Location/Qualifiers
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Mus musculus
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AY417053
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Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, Y., Shibata, Y., Shangawa, A., Shizaki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Direct Submission

J. Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; J.-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, NRI, Thttp://genome.gsc.riken.go.jp, Tax:81-45-503-9216, Plasse visit our web site (http://genome.gsc.riken.go.jp/) for further har Astaile
                                                                                                                                                                                                                                                                                                                            /tissue type="thymus"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
37. .471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MRLALLCGLLLAGITATOGGLLNINKAWTHMTGKKAFFSYWPYG
CHCGLGGKGQPKDATDWCCQKHDCCYAHLKIDGCKSLTDNYKYSISQGTIQCSDNGSW
CERQLCACDKEVALCLKQNLDSYNKRIRYYWRPRCKGKTPAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 GGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTAT 241
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Pred. No. 1e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | db xref="FANTOM DB:5830452G11"
| db xref="MG1:1909557"
| db xref="taxon:10090"
| clone="5830452G11"
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/db_xref="G1:12857530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .1582
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end: BamHI. Host: DH10B
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 501)
Marral M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACTGGCGGCCCCACTGCCGGGGGCAGACCCTGGGTGCTAGAAGCCCACACCTCT 481
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VV49h02.rl Soares thymus 2NbMT Mus musculus cDNA clone
IMAGE:1225779 5' Similar to SW:PA2M_CAVPO P47711 PHO&PHOLIPASE
MEMBRANE ASSOCIATED PRECURSOR;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                              125 ACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGC
                                                                                                                                                                                                                                                                                                                                                                   1 ACGGGGAAGAAGCCTTCTTCAGCTACTGGCCCTACGGCTGTCACTGTGGACTTGTGGGC
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constructed by Bento
                                                                                                                                                                      Gaps
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashI-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
71: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.ed<sup>11</sup>
                                                                                                                                                                      .
                                                                                                            Length
                                                                                                                                                                      Indels
  rounds of normalization, and was Soares and M.Fatima Bonaldo."
                                                                                                                                                                         93;
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High quality sequence stop: 492.
Location/Qualifiers
                                                                                                            Score 268.8; DB 9
Pred. No. 2.5e-55;
0; Mismatches 93
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Mus musculus
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                                                                                                                     45.48;
                                                                                                                        Query Match
Best Local Similarity 77.7
Matches 324; Conservative
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This read has been verified (found to hit its original self in the
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vv49h02.y1 Soares thymus 2NbMT Mus musculus cDNA clone
IMAGE:1225779 5' Similar to SW:PA2M CAVPO P47711 PHOSPHOLIPASE A2,
MEMBERANE ASSOCIATED PRECURSOR;, mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                   TACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGGCCAACCCCAAAGATGCCACG 208
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1225779"
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/lab_host="DH10B"
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Bistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tasgareishvili, R.,
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ik5a07.y1 Kaestner ngn3 wt Mus musculus cDNA 5' similar to
TR:Q9WVF6 Q9WVF6 GROUP IID SECRETED PHOSPHOLIPASE A2 ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 268.8; DB 9;
Pred. No. 2.6e-55;
0; Mismatches 93;
                                                                                                                                            /clone_lib="Soares thymus_2NbMT"
/note="Vector: pT7T3D-Pac (Pharm
                                                       clone="IMAGE:1225779"
                                     db_xref="taxon:10090"
                                                                                            tissue_type="Thymus"
                                                                                                            /dev_stage="4 weeks"
/lab_host="DH10B"
mol_type="mRNA"
strain="C57BL/6J"
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/dev_stage="D.c. 14.5"
/lab_host="E. coli-DH12S (GIBCO)"
/lab_host="E. coli-DH12S (GIBCO)"
/clocle=lorgan: pancreas, Vector: pSPORT1 (GIBCO); Site_1:
/note="Organ: pancreas, Vector: pSPORT1 (GIBCO); Site_1:
Not I: Site_2: Sal I; The library was prepared by
Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
NotI Site, and Sall linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-Sall sites in the vectors. This is one of two
libraries, ngm3 wt and ngm3 -/-. The wt library is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                     Endocrine Pancreas Consortium Tarvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
                                                                                                                                                                                                                        Email: dmelton@biohp.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For information on
Chaining a clone please contact: Dr. Marie Scearce
(mscearce@mail.med.upenn.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 456.
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                                                                                  Contact: Douglas Melton, Klaus H.
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/strain="129/Sv x CD1"
/db_xref="taxon:10090"
                   Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: ik55a07.x1
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Email: genome-reseagecriken.go.jp,

URL: http://genome-gsc.riken.go.jp,

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Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1671-1630 (2000)

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Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110051K23 product:phospholipase A2, group AKO04232
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                       Division of Experimental Animal Research in Riken contributed to
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whole body"
                                                                                                                                                                                                                                prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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High-efficiency full-length cDNA cloning
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                               Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, Y., Izawa, M., Ohara, E., Watahiki, M., Okara, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer General Connec Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60, 770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1206)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RIKEN Genome Exploration Research Group Phase II Team and the
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Matches 315; Conservative 0; Mismatches 82; 1
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WCEQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQTPGC"
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 characterization of novel mouse and human secretory
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                                                                                                                                                                                                                                                                                                                                                                /gene="PLA2"
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/replace="a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                   [bases 1 to 878]
Ishizaki,J., Suzuki,N., Higashino,K. and Hanasaki,K.
Direct Submission
Submitted [1-DEC-1998] Shionogi Research Laboratories,
Fukushima-ku, Sagisu 5-12-4, Osaka 553-0002, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 878;
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100.0%; Score 592; DB 9; L
Best Local Similarity 100.0%; Pred. No. 2.3e-139;
Matches 592; Conservative 0; Mismatches 0;
Cloning and characterization of novel mouse phospholipase A(2)s
T. Biol. Chem. 274 (35), 24973-24979 (1999) 99386983
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1. .878
                                                                                                                                                                                                                                                                          codon start=1
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/translation="MELALLCGLVVMAGVIPIQGGILNLNRMVKQVTGKMPILSYWPY
GCHCGLGGGRGQPKDATDWCCQTHDCCYDHLKTQGCSIYKDYYRYNFSQGNIHCSDKGS
WCEQQLCACDKEVAFCLKRNLDTXQKRLRFYWRPHCRGQTPGC"
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Homo sapiens phospholipase A2 (SPLASH) mRNA, complete cds.
AF188625
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Frederick, MD 21702, USA
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 1938)
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Shakhov, A.B., Rubtsov, A.V., Lyakhov, I.G., Tumanov, A.V. and Shakhov, S.A.
Nedospasov, S.A.
Direct Submission
Submitted (20-SEP-1999) Laboratory of Molecular Immunoregul IRSP, SAIC, NCI-FCRDC, P.O. Box B, Frederick, MD 21702, USF IRSP, SAIC, NOI-FCRDC, P.O. Box B, Frederick, MD 21702, USP Location/Qualifiers
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/db_xref="G1:6453793"
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codon_start=1
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Alteschul, S.F., Zeeberg, B., Buetow, K.H., Scheafer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heish, P.,
Diatchenko, L., Marulana, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratrae, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Yillalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
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249 IGACCACCTGAAGACCCAGGGGTGCAGCATCTACAAGGACTATTACAGATACAACTTTTC 308
                                              CCAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGTGAGCAGCAGCTGTGTGCCTG 360
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 2747)

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                                                                                                                                  TGACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCG
                                                                                                                                                                            369 fdacaaggaggaggagctricrgccrgaagcgcaaccrggagagcaagaagcgacrgcg
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
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                                                                                                                                                                                                                                                                                                                                                                                                                                        549 CTGGCTTTTCAAACACTCCGGGGGAGGTAGTCCCAGCCTCCCCGGGAACCC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homos sapiens phospholipase A2, group IID, mRNA (cDNA clone MGC:34386 IMAGE:5223912), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                     541 CTGGCTTTTCAAACACTCCGGGGGGGGGGTAGTCCCCAGCCTCCCCCGGAACCC
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BC025706.1 GI:19344000
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Strausberg, R.
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/note="phoslip; Region: Phospholipase A2. Phospholipase A2 releases fatty acids from the second carbon group of glycerol. Perhaps the best known members are secreted snake venoms, but also found in secreted pancreatic and membrane-associated forms. Structure is all-alpha, with two core disulfide-linked helices and a calcium-binding loop. This alignment represents the major family of PLA2s. A second minor family, defined by the honeybee venom PLA2 PDB:IPOC and related sequences from Gila monsters (Heloderma), is not recognized. This minor family different elsewhere:

//db_xref="CDD:pfam00068"
Gaithersburg, Maryland;
Web site: http://www.nisc.nth.gov/
Contact: nisc_mgcompgin.nth.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N.L., Granite,S., Gwan,X., Woong,P., Laric,P., Legaspi,R.,
Maduco,Q.L., Maniello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McClowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTCKMPILSYWPY
GCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCSIYKDYYRYNFSQGNIHCSDKGS
WCBQQLCACDKEVAFCLKRNLDTYQKRLRFYWRPHCRGQTPGC"
                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov esties: IRAK Plate: 49 Row: m Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="phospholipase A2, group IID"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
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Pred. No. 3.5e-136;
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'db_xref="LocusID:26279"
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/organism="Homo sapiens"
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245

181 185 241 305 361 425

485

301

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/codon_start=1
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/d_xref="GI:5771422"
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/translation="WRLALCGCKHDCCYAHLKIDGCKSLTDNYKYSISQGTIQCSDNGSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Memmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (basts. 1 to 1233)
Ishizaki.J., Suzuki,M., Higashino,K., Yokota,Y., Ono,T., Kawamoto,K., Fujii,M., Arita,H. and Hanasaki,K.
Cloning and characterization of novel mouse and human secretory phospholipaes A(2)s
J. Biol. Chem. 274 (35), 24973-24979 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                              GACAAGGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCGT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTACTGGCGCCCCACTGCCGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCT 481
                                                                        ATGCCTGGTGTGATTCCAATCCAGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAA 121
                                                                                                                                                           126 AIGACGGGGAAGAAGCCTICTICAGCTACTGGCCCTACGGCTGTCACTGGACTTGGT
                                                                                                                                                                                                                                                             242 GACCACCTGAAGACCCCAGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCC
                                                                                                                                                                                                                                                                                                                                                        246 ecccaccrigaagarcgarggargcaagagccrgacagacaacracaaaraacagcarcrc
                                                                                                                                                                                                                                                                                                                                                                                                    CAGGGGAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCAGCTGTGTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 GACAAGGAGGTGGCCTTGTGCTTGAAGCAAAACCTGGATAGCTACAATAAGGGCCTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GIGACIGGGAAAAIGCCCAICCICTCCIACIGGCCCIACGGCIGICACIGCGGACIAGGI
                                                                                                                                                                                                                        182 GGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTAT
9 CTGCCTGCCTTGCTCTGGGCTGGAACTATGAGACTCGCCCTGCTGTGTGGGGCTGCTGC
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Mus musculus group IID secretory phospholipase A2 (Pla2) mRNA,
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E (bases I to 1233)

In455175

S Ishizaki, J., Suzuki, N., Higashino, K. and Hanasaki, K.

Ishizaki, J., Suzuki, N., Higashino, K. and Hanasaki, K.

Direct Submission

L Submitted (11-DEC-1998) Shionogi Research Laboratories,

Fukushina-ku, Sagisu 5-12-4, Osaka 553-0002, Japan

Location/Qualifiers

1. 1233

1. 1233

Mol 1ype="MRNA"

/strain="BALB/C"

/strain="BALB/C"

/strain="BALB/C"
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|...1233
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El (bases I to 1233)

El (bases) I to 1233)

Sinizaki,J. Suzuki,N. and Hansaaki,K.

Muscas secretory phospholipase A2

Patent: JP 2000166544-A 13 20-JUN-2000;

SHONGI & CO LTD

OS Muscasculus (mouse)

PN JP 2000166544-A/13

PD 20-JUN-2000

PF 03-DEC-1998 JP 1998349602

PR JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI

PC CLINS/10,CLIZNI-91),(CLIZNI-5/09,CLIZRI-91),CLIZNI-5/00,CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91),CLIZNI-91
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                                                              AGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGAACA 311
                                                                                                                                                    TCCACTGCTCTGACAAGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAAGGAGG 371
                                     AACCCAAAGAIGCCACGGACTGGIGCIGCCAGACCCAIGACIGCIGCIAGACACCIGG 251
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Pred. No. 2.7e-64;
0; Mismatches 105; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              552 AACACTCCGGGGGGGGGGTAGTCCCAGCCTCCCCGGGAACCC
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mat_peptide (93). (467)
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1233 bp
Mouse secretory phospholipase A2.
E37214
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Mus musculus (house mouse)
Mus musculus
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ilarity 77.5%;
Conservative 0
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AUTHORS
TITLE
JOURNAL
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/codon_start=1
/product="phospholipase A2"
/protein_id="AAF42987.1"
/db_xref="G1:7239430"
/translation="MRLALLCGILLAGITATOGGILNINKMYTHMTGKKAFFSYMPYG
CHCGLGGGGPKDATDWCCQKHDCCYAHLKIDGCKSLTDNYKYSISQGTIQCSDNGSW
CBRQLCADDKBVALCLKQNLDSYNKRIRYYWRPRCKGKTPAC"
1811. 1975
/note="B1 repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF169408 2166 bp mRNA linear ROD 13-MAR-2000 Mus musculus non-secreted phospholipase A2 (Splash) mRNA, complete cds; nuclear gene for mitochondrial product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gecadadeccaacccaaagargeccacegacreerecreereccaacccarrerrerrerrer
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Shakhov, A.N., Rubtsov, A.V., Lyakhov, I.G., Tumanov, A.V. and Nedospasov, S.A.
SPIASH (PLAZIID), a novel member of phospholipase A2 family, is associated with lymphotoxin deficiency Genes Immun. 1 (3), 191-199 (2000)
11196711
                                                                                                                                                                                                                                                                                                                                                                                                                53 CIGCCIGCCTIGCTCIGGGCIGGAACTATGAGACTCGCCCTGCTGTGTGGGCTGCTGC--
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                                                                                                                                                                                                                                                                                                              Length 1975;
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                                                                                                                                                                                                                                                                                                          Score 296; DB 10; Pred. No. 2.6e-64; 0; Mismatches 105;
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    .1975
    /gene="Splash"
    .514
    /gene="Splash"

                                                                                 note="SPLASH"
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Best Local Similarity 77.5%;
Matches 372; Conservative (
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1975)
Shakhov, A.N., Rubtsov, A.V., Lyakhov, I.G., Tumanov, A.V. and
Nedospasov, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1975)
Shakhov,A.N., Rubtsov,A., Lyakhov,I.G. and Nedospasov,S.A.
Direct Submission
Submitted (16-JUL-1999) Laboratory of Molecular Immunoregulation,
IRSP, SAIC, NCI-FCRBC, Sultan Str. 560, Frederick, MD 21702, USA
Location/Qualifiers
                                                                                                                          2 CTGCCTCCACTGCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTG
                                                                                                                                                              checchectriechcheschesakchansaskhoschechensaschener
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                                                                                                Gaps
                                                                                              3;
                                                          Length 1233;
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CERQLCACDKEVALCLKQNLDSYNKRLRYYWRPRCKGKTPAC
                                                                                            Indels
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/map="between D4Mit158 and D4Mit283"
                                                      Score 296; DB 10; Pred. No. 2.7e-64; 0; Mismatches 105;
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/strain="129 x C57/B6"
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                                                    / Match
Local Similarity 77.5%;
nes 372; Conservative
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AF169407
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LOCUS

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/db_xref="d1:7230432"
/translation="WYTHMTGKGAFFSYWPYGCHCGLGGKGQPKDATDWCCQKHDCCY
AHLKIDGCKGJTDDNYKYSISQCTIQCSDNGSWCERQLCACDKEVALCLKQNLDSYNKR
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2 (bases 1 to 2166)
Shakhov,A.N., Rubtsov,A., Lyakhov,I.G. and Nedospasov,S.A.
Direct Submission
Submitted (16-JUJ-1999) Laboratory of Molecular Immunoregulation,
IRSP, SAIC, NCI-FCRDC, Sultan Str. 560, Frederick, MD 21702, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 GACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCC
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/product="non-secreted_phospholipase_A2"
                                                                                                                                                                        map="between D4Mit158 and D4Mit283"
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Seguence 533 from Patent WO0140466.
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                                                                                                /organism="Mus musculus"
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/strain=1129 x C57/B6"
/db_xref="taxon:10090"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                LRYYWRPRCKGKTPAC'
                                                                                                                                                                                                   /gene="Splash"
158. .514
/gene="Splash"
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                                                                                                                                      Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, B., Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Shewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z. Secreted and transmembrane polypeptides and nucleic acids encoding
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butel
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Best Local Similarity 97.3%; Pred. No. 2.7e-61;
Matches 289; Conservative 0; Mismatches 8;
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|mol_type="unassigned DNA"
|db xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 284.2; DB 6
Pred. No. 2.7e-61;
0; Mismatches 8
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Genentech Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: WO 0140466-A 533 07-JUN-2001;
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/db_xref="taxon:9606"
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Location/Qualifiers
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Best Local Similarity 97.3%;
Matches 289; Conservative
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Gaps

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Pred. No. 2.7e-61; 0; Mismatches 8; Indels

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1 (Basea I to 496)

2 Clark, H. F., Gurney, A. L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Dowd, P., Eaton, D., Forder, G., Grimaldi, C., Gu, C., Hass, P. E., Heldens, S., Huang, A., Kim, H.S., Klimwoski, L., Jin, Y., Johnson, S., Schoenfeld, J., Seshagiri, S., Simmonski, L., Singh, J., Shonson, S., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K. Kie, M. H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:

M. Bloinformatics Assessment

M. Genome Res. 13 (10), 2265-2270 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                  PRI 03-OCT-2003 complete cds.
                                                              61 GAIGGCIGGIGIGATICCAATCCAGGGCGGGAICCTGAACCTGAACAAGATGGTCAAGCA 120
                                                                                                                                  121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180
                                                                                                                                                                  121 AGTGACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180
                                                                                                                                                                                                    181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
                                                                                       181 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
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GCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLM
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                                                                                                                                                                                                                                                                     241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
                                                                                                                                                                                                                                                                                          241 TGACCACCTGAAGACCCAGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCAT 297
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CA 94080, USA
                   1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTTGGTGGTGT
TCTGCCTCCACTGCTCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                       496 bp mRNA linear
Homo sapiens clone DNA76538 PLA2G2D (UNQ768) mRNA,
AY358606
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Submitted (01-AUG-2003) Department of
Inc., 1 DNA Way, South San Francisco,
Location/Qualifiers
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DNA76538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="UNQ768"
29. .379
/locus_tag="UNQ768"
/note="PR01561"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="PLA2G2D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY358606.1 GI:37182333
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Homo sapiens (human)
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48.0%; Score 284.2; DB 9; Length 496;

Query Match

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AF124374 904 bp mRNA linear ROD 06-JUL-1999
Mus musculus group IID secreted phospholipase A2 (Plaza2) mRNA,
             120
                                  61 GATGGCTGGTGATTCCAATCCAGGGGGGATCCTGAACCTGAACAAGATGGTCAAGGT 120
                                                                                                              180
                                                                                                                                   TGGCAGAGGCCAACCCAAAGATGCCACGGACTGCTGCTGCCAGACCCATGACTGCTGCTA 240
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CHCGLGGKKQPKDATDWCCQKHDCCYAHLKIDGCKSLTDNYKYSISQGTIQCSDNGSW
CERQLCACDKEVALCLKQNLDSYNKRLRYYMRPRCKGKTPAC"
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Valentin, E., Koduri, R.S., Scimeca, J.C., Carle, G., Gelb, M.H., Lazdunski, M. and Lambeau, G.
                                                                                                                                                                                                                                       121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGCTAGG
                                                                                                                                                                                                                                                                                                      TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
                                                                                                                                                                                                                                                                                                                                   61 GATGGCTGGTGTTCCAATCCAGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA
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Valentin, E., Koduri, R.S., Scimeca, J.C., Carle, G., Gelb, M.H.,
Lazdunski, M. and Lambeau, G.
Direct Submission
Submitted (28-JAN-1999) CNRS, IPMC, Sophia Antipolis, 660 rc
Lucioles, Valbonne 06560, France
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10. .444
/gene="Pla2a2"
/EC_number="3.1.1.4"
/note="Ca2+-dependent secreted phospholipase A2"
/codon_start=1
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/protein_id="AAD42773.1"
/db_xref="GI:5359708"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phospholipase A2
J. Biol. Chem. 274 (27), 19152-19160 (1999)
99315857
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/db_xref="taxon:10090"
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1. .904
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Mus musculus
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Best Local Similarity
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us-09-830-321a-4.rge

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on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl RPI-169023 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                     IMPORTANT: This sequence is not the entire insert of clone RPI-169023 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RPI-169023 is at 1 in this sequence. The true left end of clone RPI-340NI is at 98644 in this sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781. .909
/note="MER65-internal repeat: matches 1665. .1801 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2537. .2705 of consensus"
8984. .9131
/note="L2 repeat: matches 2414. .2576 of consensus"
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/note="MER4-internal repeat: matches 6087. .6596 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1897. .2592
/note="MER4-internal repeat: matches 2472. .3484 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat: matches 228. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30. .756
note="MBRR83-internal repeat: matches 1668. .1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     656. .1896
note="LTR8 repeat: matches 1. .257 of consensus"
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note="MER4-internal repeat: matches 3484. .3679
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'hote="MER4-internal repeat: matches 3840.
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/note="MER4-internal repeat: matches 1764.
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/note="LIMC2 repeat: matches 6050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7800. .8099
/note="L1M4 repeat: matches 5497.
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note="MLT1E repeat: matches 507.
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/note="MER4A2 repeat: matches 1.
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/note="match: GSS: Em:AQ263839"
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/note="match: GSS: Em:AQ591805"
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/note="match: STS: Em:G50772
match: GSS: Em:AQ201252"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="1"
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/note="THE1B repeat:
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/clone_lib="RPCI-1"
107. .371
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Wallis, J.

Wallis, J.

Direct Submission

Submitted (25-CT-2000) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (25-CT-2000) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (25-CT-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonereques@sanger.ac.uk

or Aug 14, 2000 this sequence version replaced gi:9714699.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation amnotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map criteria annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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Catarrhini, Hominidae, Homo.
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Homo sapiens (human)
Homo sapiens
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Mammalia, Eutheria, Primates,
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CIZN9/16,CIZNS/10,CIZN15/09,CIZQI/44,G01N33/15//(CIZN9/16, PC
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Ishizaki,J., Suzuki,N. and Hanasaki,K.
Mouse scretcry phospholipase A2
Patent: 97 2001065544-A 1 20-JUN-2000,
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/note="match: GSS: Em:AQ743836"
22535. .22832
/note="AluJb repeat: matches 3. .312 of consensus"
22849. .23054
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45.9%; Score 272; DB 9; )
Best Local Similarity 100.0%; Pred. No. 2.8e-58;
Matches 272; Conservative 0; Mismatches 0;
                          note="AluSx repeat: matches 1.
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JP 2000166544-A/1.
Mus musculus (house mouse)
Mus musculus
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JP 2000166544-A/1
20-JUN-2000
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PN JP 20
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PF 09-DE
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C12R1:91)
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/ 10.53... ...1.5380

join(12774. ...12834,16626. ...16744,22015. ...22080,44003. .44308)

/ 10.59ne="40169023.2"

/ 10.50ne="40169023.2"

/ 10.50e="40169023.2"

/ 10.50e="40169023.2"

/ 10.50e="40169023.2.1 (novel protein)"

/ 10.50e="40169023.2.1 (novel protein)"

/ 10.50e="40169023.2.1 (novel protein)"

/ 10.50e="40169023.2.1 (novel protein)"

/ 10.50e="401694"

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17754. 17885
17754. 17885
17754. 17885
17754. 17885
17768. 18857
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18858 repeat: matches 10. 109 of consensus"
18854. 18858
18854. 18895
19854. 18958
19854. 19128
19139. 19128
19139. 19511
19139. 19511
                                                                                   .-544 of consensus"
                                 .6327 of consensus"
                                                                                                                                                                                                                        /note="Alusx repeat: matches 5. .276 of consensus"
10937. .10951
10939. .11702
10939. .11702
10233. .1288
12233. .12588
                                                                                                  1520. 10539 ... matches 2963. 3988 of consensus (0553. 10664
                                                                                                                                            note="5' UTR probably continues in bA66M4 (AL360079) rd exon misses correct 3' splice site"
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/note="LiM4 repeat: matches 4735. .4751 of consensus" 20548. .20844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Aluub repeat: matches 3. 307 of consensus" 2500. 15387 repeat: matches 1. 426 of consensus" 1554. 15790 repeat: matches 1. .133 of consensus" note="Aluuo repeat: matches 1. .133 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9567. .19724 .
hote="MERG3 repeat: matches 1. .783 of consensus"
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note="AluJb repeat: matches 2. .297 of consensus"
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/evidence=not experimental
/product="du169053.2.1" (novel protein)"
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/db_xref="G1:10862734"
/db_xref="SPREMBL:09H507"
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1734..17743
                                                 9376. .9483
/note="L1PA13 repeat: matches -651.
244 .9359
note="LiMC1 repeat: matches 6210.
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/organism="unknown"
                                                                                                                                     54. .113
114. .488
/product="unnamed"
55. .557
744. .749
                                                                                                                                                                                                                                                                                                                                                                                                                                206 ACGGACTGGTGCTGCCAGACCCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17 from patent AR274880
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Best Local Similarity 55.5
Matches 258; Conservative
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mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cavia porcellus
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vial, D., Senorale-Pose, M., Havet, N., Molio, L., Vargaftig, B.B. and
                                                                                                                                                                               9
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Submitted (10-NOV-1994) D. Vial, Institut Pasteur, 25 rue du Dr.
Roux, 75015 Paris, FRANCE
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417
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                                                                                                       Length 501;
/organism='Mus musculus (mouse)'
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C.porcellus mRNA for typeII phospholipase A2.
X82631
                                                                                                                               93; Indels
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/cell type="alveolar macrophage"
/dev_stage="adult"
                                                                                                       DB 6;
                                                                                                       Score 268.8; DB 6 Pred. No. 2.2e-57;
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phospholipase a2.
Cavia porcellus (domestic guinea pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 760
/organism="Cavia porcellus"
/mol_type="mRNA"
/strain="Hartley"
                                                                                                                                  0; Mismatches
                                          organism="Mus musculus"
                                                      /mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                          45.48;
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Vial, D.
                                                                                                                                  Conservative
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CPIIPHA2
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PAT 10-APR-2003
54. .491

CE number="3.1.1.4"

/codon_start=1
/product="typeII phospholipase A2"

/protein id="CAA57953.1"

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/db_xref="G9MISS-PROT: P47711"

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GCHCGYGGREPRADTRGCVPHDCCYDRLMKRGCGTKFLNYRFTHKGSSITCSVKQN
SCQKQLCECDKAAAYCFAANLKSYSRRYQFYNGLCRGKTPSC"
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Pred. No. 3.7e-23;
0; Mismatches 207;
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/mol_type="genomic DNA"

ORIGIN

67 IGGIGIGATICCAAICCAAGGCGGGAICCIGAACCIGAACAAGAIGGICAAGGIGAC 126 127 IGGGAAAAIGCCCAICCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG 186 231 AGGGAAGAACGCCCTGACAACTACGGCTTCTACGGCTGTTACTGCGGCTGGTGGGGCGCCG 290 247 CCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATACAGATACAACTTTTCCCAGGG 306 351 GCTGGAGGAGAAGGGCTGCAACATTCGCACACTCCTACAATACAGATTCGCGTGGGG 410 367 GGAGGTGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCGTTTCTA 426 468 GAAGCTCGTCTACTGCCTCAAGAGAAACCTACGGAGCTACAAACCCACAGTACCAATACTT 527 3; Gaps Query Match 20.2%; Score 119.6; DB 6; Length 1016; Best Local Similarity 58.0%; Pred. No. 1.5e-19; Matches 231; Conservative 0; Mismatches 164; Indels 3; 427 CTGGCGGCCCCACTGCCGGGGCAGACCCCTGGGTGCT 464 528 TCCCAACATCCTCTGCTCCTAGGCCTCCCCAGGGAGCT 565 Dp qq ò δ Db ò qq à g ď g

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7, 2004, 11:14:15; Search time 251.748 Seconds (without alignments) 9989.875 Million cell updates/sec October Run on:

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Title: Perfect score: Sednence:

1 tetgeetecactgetetgtg........5ecageetececeggaace 592 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 seqs, 2124099041 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

N Geneseq 29Jan04:*

1: geneseqn1980s:*
2: geneseqn200s:*
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And the property of the proper Aaa72076 CDNA enco Aa477684 Human PRO Aaf54466 DNA encod Aas21510 Human CDN Acd24119 Novel hum Aca67260 CDNA enco Abx89407 DNA encod Aaa53269 Human pho Human sec Human cDN Human PRO Human PRO Homo sapi Novel hum Novel Description Ada76483 F Ada19133 F Ada61756 F Adb19541 N Acd42061 Aca04290 SUMMARIES AAS14884 AAH98759 AAH99768 AAD19218 AAA53269 AAA60878 AAA60866 AAA72076 AAA77684 AAF54466 AAS21510 ACD24119 ACD42061 ACA04290 ADA46052 ADA76483 ACA03869 ABX89407 ADA19133 ADA61756 ADB19541 ACC72857 Query Match Length DB 592 878 2747 1927 1927 11931 1233 1233 496 100.0 Score No.

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ALIGNMENTS

T 1 269 AAA53269 standard; cDNA; 592 BP. AAA53269; 05-OCT-2000 (first entry) Human phospholipase 1 HPPL1 coding sequence.	<pre>Human; phospholipase 1; HPPL1; cancer; autoimmune disorder; inflammatory disorder; reproductive disorder; infection; ss. Homo sapiens.</pre>	Key Location/Qualifiers CDS 29466 /*tag= a /product= "HPPL1"	/*tag= b /note= "this is a putative signal 2976 //tag= c /note= "this is a putative signal	63 "this is a 63	-A2.		illman JL, Bandman O, Guegler KJ, Corley NC, Baughn MR; zimzai Y, Lal P, Lu DAM;
RESULT 1 AAA53269 ID AAA532 XX AC AAA532 XX XX XX DT 05-OCT XX XX XX XX XX XX	Human; inflami Homo s	Key CDS	sig per	mat_peg mat_peg	WO20002	27-0CT- 27-0CT- 21-JAN- (INCY-)	Hillman Azimzai
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AAA60878 standard; cDNA; 878

or

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The present sequence is the coding sequence of human phospholipase 1

(HPPLI). The protein produced from this sequence is involved in the hydrolysis of membrane phospholipids. The protein and its coding sequence to hydrolysis of membrane phospholipids. The protein and its coding sequence can be used to diagnose and treat the following: cancers such as prostate, breast and testicular cancers, autoimmune and inflammatory disorders such as ALDS, allergies, anaemia, asthma, atherosclerosis, crohn's disease, diabetes mellitus, emphysema, Graves' disease, irritable commatoid arthritis and systemic lupus erythematosus, infection caused by viruses, fungi, bacteria, parasites and protozoa, and reproductive disorders including infertility, disruptions of the menstrual cycle, polycystic ovary syndrome, ectopic pregnancies, disruptions of spermatogenesis, cancers within the reproductive tract and impotence. This coding sequence was obtained from clone no.2641779, which was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human phospholipase genes and proteins useful to diagnose, prevent treat cancer, autoimmune or inflammatory or reproductive disorders.
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                                                                                                               Claim 9; Page 74; 80pp; English.
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WPI; 2000-350750/30
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Best Local Similarity
                     P-PSDB; AAB03627
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Human secretory phospholipase A2 (PLA2) and its encoded gene for diagnosis and treatment of secretory PLA2-associated diseases e.g. septic shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid arthritis.
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                                                                                                                                                                                                          Secretory phospholipase A2; PLA2; antiallergic; antinflammatory; antibacterial; immunosuppressive; tranquillser; vulnerary; antirheumatic; antiarthritic; septic shock; trauma; pancreatitis; allergic rhinitis; chronic rheumatoid arthritis; ss.
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100.0%; Pred. No. 3.3e-149;
iive 0; Mismatches 0;
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29. .466
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P-PSDB; AAB12537.
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TGGCAGAGGCCAAACCCCAAAGATGCCACGGACTGCTGCCAGACCCCATGACTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
heart disease; atherosclerosis; endometriosis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genes that are up-regulated or down-regulated in cancers, useful a markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                                                                               CTGGCTTTTCAAACACTCCGGGGGGGGGTAGTCCCAGCCTCCCCCGGAACCC 592
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                                                                                                                                                                                                                                                                                                                                                                                                         ACC72857 standard; cDNA; 2747 BP
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20-SEP-2001; 2001US-0323887P.
13-NOV-2001; 2001US-0350666P.
08-FEB-2002; 2002US-0355145P.
08-FEB-2002; 2002US-035257P.
12-APR-2002; 2002US-0372246P.
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Zlotnik A;
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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-

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acute lymphocytic leukemia). ACC72681 to ACC72880 represent cancer related gene mucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cellin a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a drug screening assay. The nucleic acid is useful as dispussing a pathology, e.g. cancer (e.g. cancer of the bone marrow, the rapeutic targets. In particular, the nucleic acid is useful for banceas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in a pathology, particularly for identifying agents for treating these
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   genes up-regulated in
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                                                                                                                                                                                                                                                                                              Sequence 2747 BP; 719 A; 762 C; 668 G; 598 T; 0 U; 0 Other;
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regulated in specific cancers (e.g. about 1031
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M antiarthritic; cytostatic; antiarteriosoclerotic; vulnerary,

M neuroprotective, nootropic; antiarteriosoclerotic; vulnerary,

M neuroprotective, nootropic; antiarteriosoclerotic; vasotropic; cardiant;

KW anti-inflammatory; antibacterial; antiporiatic; thyromimetic;

M municompoulator; antiseborrheic; dermatological; thyromimetic;

KW antiniflammatory; antiseborrheic; dermatological; vasoconstriction;

KW astrointestinal disorder; cardiovascular disorder; hypertension;

KW gastrointestinal disorder; cardiovascular disorder; hypertension;

KW coronary heart disease; arteriosoclerosis; anorexia; obesity; bulimia;

KW coronary heart disease; plumonary system disorder;

KW hyperproliferative disease; plumonary system disorder;

KW huntington's disease; schizophrenia; mania; dementia; paramoia;

KW psychosis; autism; sleep disorder; immune system disorder;

KW psychosis; autism; alepe disorder; immune system disorder;

KW multiple sclerosis; ischaemic brain injury; stroke; infectious disease;

KW diabetes mellitus; munuological disorder; pennatoid arthritis;

M adubtes mellitus; immunological disorder; pennatoid arthritis;

M mintiple sclerosis; ischaemic brain injury; stroke; infectious disease;

KW minamatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;

KW neural system disorder; respiratory disorder; olfactory disorder;

KW neural system disorder; respiratory disorder; olfactory disorder;
                                                                                                                     novel human protein; NHP; ss; antidiabetic; antirheumatic;
Human cDNA encoding novel human protein NHP #5
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ಹ .459 /*tag= Homo sapiens.

Location/Qualifiers /product= "NHP #5"

WO200174896-A1

11-OCT-2001

02-APR-2001; 2001WO-US010542.

03-APR-2000; 2000US-0194118P. 29-SEP-2000; 2000US-0236384P.

(HUMA-) HUMAN GENOME SCI INC

Gentz RL, Endress GA; Coleman TA, Soppet DR, Moore PA, Ni J, Li Y, Dillon PJ;

WPI; 2001-626394/72. P-PSDB; AAU09096 New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular disorders, autoimmune disorders and reproductive disorders.

Claim 1; Page 294; 318pp; English.

that encode them and antibodies raised against them. The proteins,
antibodies and nucleic acids are useful in the diagnosis, prognosis,
antibodies and nucleic acids are useful in the diagnosis, prognosis,
prevention and/or treatment or diseases and/or disorders involving
prevention and/or treatment or diseases and/or disorders involving
construction, gastrointestinal disorders, cardiovascular disorders
(e.g. hypertension, erectile dysfunction, high blood pressure, coronary
cachexia, disorders of small intestine, disorders of reproductive system
(e.g. male infertility and/or impotence), testicular cancer, lung tumours
and other hyperproliferative disorders, disorders of pulmonary system,
central nervous system disorders (e.g. Alzheimer's disease, Parkinson's
disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,
panic disorder, learning disabilities, amyotropic lateral sclerosis,
psychoses, autism, sleep disorders), immune system disorders (e.g. invention relates to novel human proteins (NHP) and the nucleic acids

Homo sapiens

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Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
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                                                                                                                                                                                                                                                    75
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            central nervous system disorders (e.g. multiple sclerosis, ischaemic brain injury and/or stroke), infectious diseases, diabetes mellitus, immunological disorders (e.g. asthma, acquired immunodeficient syndrome (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, psoriasis and lupus erythematosus), neural system disorders, respiratory disorders, olfactory disorders and wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429 CCACTGCCGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCCTCTACCTTGTTCTCAG
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Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,
                                                                                                                                                                                                                      Gabs
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                                                                                                                                                                                   Length 854;
                                                                                                                                                Sequence 854 BP; 186 A; 254 C; 238 G; 176 T; 0 U; 0 Other;
                                                                                                                                                                                                                      Indels
                                                                                                               The present sequence encodes an NHP of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCCGGGGGGAGGTAGTCCCAGCCTCCCCCGGAACCC 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human EST-derived coding sequence SEQ ID NO: 616.
                                                                                                                                                                                   Score 575.4; DB 4;
Pred. No. 9.5e-145;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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Matches 576; Conservative
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AAH99768
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                                                                                                                                                                          Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                        96.1%; Score 568.8; DB 4; Length 1927; 98.8%; Pred. No. 7.4e-143; tive 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                     Sequence 1927 BP; 413 A; 598 C; 480 G; 436 T; 0 U; 0 Other;
                                                                                                                        Chen R,
                                                                                                                      u P, Qian XB, Wang Z,
Zhang J, Werhman T;
                                                                                                                                                                                                   Claim 1; Page 599-600; 1275pp; English.
                                                              17-JUL-2000; 2000US-00617746
03-AUG-2000; 2000US-00631451
15-SEP-2000; 2000US-00663870.
                                    25-JAN-2001; 2001WO-US002687
                                                       2000US-00491404
                                                                                                                      Zhou P,
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                     , Liu C, Zho
Drmanac RA,
                                                                                                                                                2001-476164/51
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                       P-PSDB; AAM24100
                                                                                                                                                                                                                                                                                     of the invention
WO200154477-A2
                                                     25-JAN-2000;
                   02-AUG-2001
                                                                                                                                                                                                                                                                                                                                          Matches 573;
                                                                                                                     Tang YT,
                                                                                                                                                                                                                                                                                                                         Query Match
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AAM199166 to AAM199904 encode the human proteins given in AAM25225 to
AAM25963. The proteins can have activities based on the tissues and cells
they are expressed in, such as: antiinflammatory; antirheumatic;
antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary;
cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary;
antiulcer; osteopathic; dermatological; antiallergic; antiathmatic;
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
cantiparkinsonian; and immunostimulant. The proteins and polynucleotides
cencoding them can be used in gene therapy, antisense therapy and vaccine
production, The proteins and polynucleotides are useful for screening for
cording them can be used in gene therapy, antisense therapy and vaccine
production, The proteins and polynucleotides are useful for screening for
cordisorders associated with the activity of a protein e.g. inflammation,
theumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
cheumatodid arthritis, septic shock, pancreatitis, cardiac dysfunction,
infections, autoimmunity, genetic diseases, haematopoietic disorders,
482 CAGCATGGAGCTCTGGCATCCCCACCTCAGTATCTAACCTGAACCAGCCTGGCTTTTTCAA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinfemantory; antirheumatic; antiarthritic; immunosuppressive; antiinfemantory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antialtery; fungicide; antimutegen; cardiavascular; antianaemic; anaemia; dermatological; antialteryic; untiasthmatic; antidiabetic; cezema; neuropprotective; antidepressant; noctropic; antidiabetic; cytostatic; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancratitis; cardiac dystunction; neuropathology; cardiac anaphylaxis; autoimmunity; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; alleryic rhinitis; diabetes; multiple sclerosis, depression;
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease; Parkinson's disease; neurodegenerative disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein encoding cDNA sequence SEQ ID NO:603
                                                                                                                                                                                          542 ACACTCCGGGGGGGGGTAGTCCCAGCCTCCCCCGGAACCC
                                                                                                    553 ACACTCCGGGGGGAGGTAGTCCCAGCCTCCCCGGAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH99768 standard; cDNA; 1927 BP
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
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The invention relates to polymucleotides encoding proteins CG122, CG179, CG151, CG162, CG27, CG153 and CG168 which are related to proteins CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins involved in lipid metabolism and cardiovascular diseases such as human capolisportetins, lipases and lipoprotein receptor Proteins. These DNA and protein sequences are useful for treating or preventing disorders protein sequences are useful for treating lipid metabolism, cardiovascular diseases and corpression and for treating lipid metabolism, cardiovascular diseases and the presence of or predisposition to a disease associated with altered the presence of or predisposition to a disease associated with altered corpressing Allr proteins are useful for identifying a hardpentic agent expressing Allr proteins are useful for identifying a hardpentic agent corpressing Allr proteins are useful for identifying a hardpentic of physiological interactions of this polypeptide. Vectors comprising these physiological interactions of this polypeptide. Vectors comprising these corpressing Allr sequences are also useful for producing Allr proteins. The mutaneous comprising Allr proteins corpressing and protein sequences of this polypeptide. Vectors comprising these corpressing and protein sequences are also useful for producing Allr proteins. The meaning and crebral artery thrombosis and crebral artery thrombosis or intracardiac corpressing themselves artery thrombosis and stroke. The nucleotides of the invention are used in gene therapy. The present sequence is human CG95 (or C870) lipase DNA
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Drmanac RT, Ren F,
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The present invention describes human secretory phospholipase A2 (PLA2). PLA2 has antiallergic, antiinflammatory, antibacterial, tranquillser, immunosuppressive, vulnerary, antirheumatic and antiarthritic activities. Human secretory phospholipase A2 (FLA2), the gene encoding it and antibodies against it are useful for the diagnosis and treatment of secretory PLA2-associated diseases e.g. septic shock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid arthritis. The present sequence encodes mouse PLA2, which is used in an example from the present invention
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                       Human secretory phospholipase A2 (PLA2) and its encoded gene for diagnosis and treatment of secretory PLA2-associated diseases e.g. segshock, trauma, pancreatitis, allergic rhinitis and chronic rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1233 BP; 279 A; 337 C; 307 G; 310 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 296; DB 3;
Pred. No. 1.7e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding mouse secreted phospholipase A2
                                                                                                                                                    Example 3; Page 35-36; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Best Local Similarity 77.5%;
Matches 372; Conservative
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                                                                          shock, tra
arthritis.
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                                                                                                                                                                                                                 324 ACAAGGGAAGCTGGTGTGAGCAGCTGTGTGCCTGTGACAAGGAGGTGGCCTTCTGCC
                                                                                                                  GCGGCATCTACAAGACTATTACAGATACAACTTTTCCCAGGGGAACATCCACTGCTCTG
                                                                                                                                                                                                                                                                                                                      TGAAGCGCAACCTGGACACCTACCAGAAGCGACTGCGTTTCTACTGGCGGCCCCACTGCC
                                                                                                                                                                                                                                                                                                                                                                                                              444 GGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCCTCTACCCTGTTCCTCAGCATGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse secretory phospholipase A2 nucleotide sequence SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product= "secretory phospholipase A2 (PLA2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA60866 standard; cDNA; 1233
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/*tag= c
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/*tag= b
93. .467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-423429/36.
P-PSDB; AAB12536.
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AAA60866 RESULT

125 181 185 241 245 301 305 361 365 421

99

Gaps

3;

Indels

Length 1233;

425

481 485 us-09-830-321a-4.rng

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, Ferrara N,
r, Gurney AL,
Williams PM,
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99US-0123957P.
99US-0131445P.
99US-0134287P.
99WO-US012252.
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99WO-US023089
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                                                                                                                   AAA77684 standard; cDNA; 496
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lowski PJ,
                                                                                                                                                                                                            (first entry)
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Godowski
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                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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02-JUN-1999;
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26-JUL-1999;
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                                                                                                                                                                   AAA77684;
           426
                                                                              RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents cDNA encoding a mouse secreted phospholipase A2 (secreted PLA2). This was initially identified in an EST (expressed sequence tag) database, and a fragment (AAA72077) was isolated from CDNA derived from several mouse tissue types using primers AAA72078-A72081.
The full length cDNA was generated with primers AAA72078-A72081. Invention relates to the novel secreted PLA2, nucleic acids encoding it, and variants of the protein which retain phospholipase A2 activity. It also encompasses an expression vector and host cells comprising DNA encoding murine secreted PLA2, a method for the recombinant production of the protein, a method of screening potential inhibitors of the protein and the compounds thus identified, and an antibody specific for murine PLA2. The antibody can be used for the diagnosis of a variety of diseases
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                                                                                                                            "Mouse mature secreted phospholipase A2"
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                "Mouse secreted phospholipase A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 105; Indels
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Pred. No. 1.7e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse secretion type phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Page 8-10; 12pp; Japanese
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77.5%;
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/product= ".36..92
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Best Local Similarity 77.5
Matches 372; Conservative
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                                                                                     93. .467
/*tag= c
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                                                                                                                                                                                   JP2000166544-A.
                                                                                                                                                                                                                                                                      09-DEC-1998;
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                                                  sig_peptide
                                                                                            mat_peptide
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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy. For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA7721 and AAB2438B to AAB24435 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine; ss.
Nucleic acids encoding PRO polypeptides useful for preventing, diagnand treating diagnosing a cardiovascular, endothelial or anglogenic disorders in mammals.
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Kuo SS, Pa
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Klein RD,
Wood WI;
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The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy
                                                                                                                                                                                                                                                                                                                                               61 GAIGGCIGGIGIGATICCAAICCAGGGGGGGAICCIGAACCIGAACAAGAIGGICAAGCA 120
                                                                                                                                                                                                                                                                                                                                                                 61 GATGGCTGGTGATTCCAATCCAGGGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCTGCCTCCACTGCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGGGGTGGTGGTGGT
                                                                                                                                                                                                                                                                                                        Score 284.2; DB 4; Length 496; Pred. No. 1.9e-66; 0; Mismatches 8; Indels 0
                                                                                                                                                                                   Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA sequence encoding for PR01561 polypeptide.
                               Claim 2; Fig 217; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS21510 standard; cDNA; 496 BP
                                                                                                                                                                                                                       48.0%;
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30-DEC-1999; 99WO-US031243
30-DEC-1999; 99WO-US031274.
05-JAN-2000; 2000WO-US0002194.
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99WO-US030911
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                                                                                                                                                                                                                                                     289; Conservative
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01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
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20-DEC-1999;
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Hillan KJ;
Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                             241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene
                                                                                                                                         1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGGGGTGGTGGTGGTGGTGGTGGTGGTGGT
                                                                                                                                                              121 AGTGACTGGGAAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGG
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                                                                                                                     Gaps
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                                                                              48.0%; Score 284.2; DB 3; Length 496; 97.3%; Pred. No. 1.9e-66; Live 0; Mismatches 8; Indels 0
   protein sequences used in the exemplification
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A, Tumas D,
                                            Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Botstein D, Desnoyers L, Baton DL, Fr
ddard A, Godowski PJ, Grimaldi CJ, Gui
oni NF, Roy MA, Smith V, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding protein of the invention #109.
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99US-0144758P.
99US-0145698P.
99WO-US020111.
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99WO-US028551.
99WO-US030095.
2000WO-US000219.
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                                                                                                               Conservative
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Pan J, Paoni NF, Roy
Williams PM, Wood WI;
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                                                                         Query Match
Best Local Similarity
Matches 289; Conserv
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nucleotide and propresent invention
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16-DEC-1999;
05-JAN-2000;
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01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
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20-JUL-1999;
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RESULT 11

AAF54466

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AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, colon, properide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour of heorosis factor-alpha (TNP-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or apen expression in periosis factor eels; the release of proteoglycans from cartilage, the release of proteoglycans from cartilage, the cells, the release of proteoglycans from cartilage, the coloriferation of inner ear utricular supporting cells or of T-coloriferation of inner ear utricular supporting cells or of T-coloriferation of inner ear utricular supporting cells or of T-coloriferation of monocytes (PBMCS), or the proliferation of endothelial cells. Some of the PRO colypeptides may modulate glucose or free fatty acid uptake by skeletal colypeptides may modulate glucose or free fatty acid uptake by skeletal colypeptides can be used in assays to identify molecules involved in binding interactions. The prolymucleotides encoding PRO colypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deforge L, Desnoyers L, Filvaroff E, G
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;
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ME, Goddard A, Godowf
Stewart TA, Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000; 2000WO-US020710.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
                                                                                                                                                                                                                      15-MAR-2000; 2000WO-US006884.
20-MAR-2000; 2000WO-US007377.
21-MAR-2000; 2000WO-US007532.
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                                                                                                                                                                  02-MAR-2000; 2000WO-US005841.
03-MAR-2000; 2000US-0187202P.
10-MAR-2000; 2000WO-US006319.
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2000US-0209832P.
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                                                                                       2000WO-US004414.
                                                                      2000WO-US004342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    breast, prostate, cervical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-408281/43.
P-PSDB; AAU12438.
                                 11-FEB-2000; 2
18-FEB-2000; 2
18-FEB-2000; 2
18-FEB-2000; 2
24-FEB-2000; 2
24-FEB-2000; 2
01-MAR-2000; 2
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Smith V, Ste
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30-MAY-2000;
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06-JAN-2000;
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Gao W;

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Human; secreted and transmembrane protein; PRO; antiinflammatory; antidabetic; cardiant; anti-infertility; anti-HIV; cytostatic; antidabetic; gene therapy; tumour necrosis factor (TMF)-alpha release; rell proliferation; cell differentiation; gene expression modulator; proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; atherosclerosis; acrdired immunodeficiency syndrome; cancer; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; bioreactor; tissue typing; gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing; gene; ss.
                                                                                                                     TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA 240
                                                                      121 AGIGACIGGGAAAAIGCCCAICCICICTACIGGCCCTACGGGCIGICACIGCGGACIAGG 180
                                                                                     241 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
                                                                                                                                                                                            TGACCACCTGAAGACCCAGGGTGCGGCATCTACAAGGACAACAACAAAAAGCAGCAT 297
1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGT
                         61 GATGGCTGGTGTTCCAATCCAGGGGGGATCCTGAACCTGAACAAGATGGTCAAGGA
                                                                                                                                                                                                                                                                                                                             Novel human secreted and transmembrane protein PR01561 cDNA.
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98WO-US014552
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16-SEP-1998;
17-SEP-1998;
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Gaps

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Query Match

48.0%; Score 284.2; DB 4; Length 496;
Best Local Similarity 97.3%; Pred. No. 1.9e-66;
Matches 289; Conservative 0; Mismatches 8; Indels 0;

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2001US-00816744.
2001US-00828366.
2001US-00854208.
2001US-00854280.
                                      99WO-US028301
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2001US-00872035.
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99WO-US030911
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 99WO-US021547
99WO-US023089
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                       99WO-US028313
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2001US-00808689.
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2001US-00887879
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18-FEB-2000;
22-FEB-2000;
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20-DEC-2000;
20-DEC-2000;
20-DEC-2000;
                     30-NOV-1999;
30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
16-DEC-1999;
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21-JUN-2001;
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06-JAN-2000;
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24-FEB-2000;
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02-MAR-2000;
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09-AUG-2001;
16-AUG-2001;
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22-MAR-2001;
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18-MAY-2001;
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25-MAY-2001;
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                                                                                           20-DEC-:
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The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a cet propeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF) -alpha from human blood, modulate the proliferation or differentiation of cells, stimulate or inhibit the printiate the release of proteoglycans, stimulate the release of cytokine of from peripheral blood mononuclear cells, inhibit the binding of A-peptide from peripheral blood mononuclear cells, inhibit the binding of A-peptide or diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome caid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome and pubbridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, cribs sequence encodes a novel human secreted and transmembrane PRO
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                                                                                                                                                                                                                                                       New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency syndrome (AIDS), or cancer.
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                                                                                            Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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48.0%; Score 284.2; DB 7; Length 496;
Best Local Similarity 97.3%; Pred. No. 1.9e-66;
Matches 289; Conservative 0; Mismatches 8; Indels 0;
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  19-DEC-2001; 2001US-00028072.
                                                                                         Baker KP, Beresini M,
Gerritsen ME, Goddard
Smith V, Stewart TA,
                                              (GETH ) GENENTECH INC.
                                                                                                                                       Stewart TA,
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P-PSDB; ABO17882.
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ACA67260 standard; cDNA; 496 BP.

RESULT 14 ACA67260 ACA67260;

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Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; diabetes; bone disorder; cartilage disorder; rhematoid arthrifs; obesity; sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia; hearing loss; coaqulation disorder; stroke; heart attack; cardiant; antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic; antirheumatic; auditory; cerebroprotective; anglogenic; gene; ss.
                        cDNA encoding human PRO polypeptide #267.
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9705-005287P.
9705-0052287P.
9705-0052287P.
9705-0052816P.
9705-0053127P.
9705-0053127P.
9705-0053127P.
9705-0063127P.
9705-0063127P.
9705-0063128P.
9705-0063128P.
9705-0063138P.
9705-0063138P.
9705-0063138P.
9705-0063738P.
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98WO-US012456.
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97US-0059122P.
97US-0059184P.
97US-0059263P.
97US-0059352P.
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97US-0056974P.
97US-0059113P.
97US-0059115P.
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          23-JUN-2003 (first entry)
                                                                                                                 US2003004311-A1.
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17-0CT-1997;
17-0CT-1997;
24-0CT-1997;
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24-0CT-1997;
24-0CT-1997;
27-0CT-1997;
27-0CT-1997;
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-MAR-1998;
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28-0CT-1997;
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                                                                                                   Homo sapiens
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07-NOV-1997
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09-FEB-1998
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obseity, hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated PRO polypeptide useful for treating diabetes, rheumatoid arthritis, sports injuries, obesity, hearing loss in mammals, stroke, heart attack.
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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99WO-US030095.
99WO-US030911.
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22-FBB-2000; 2000WO-US004414.
24-FBB-2000; 2000WO-TOO.
24-FBB-2000; 2000WO-TOO.
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06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
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2000WO-US005004
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         Serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ACA66994-ACA67268 represent cDNA sequences encoding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
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                                                                                                                                                           GATGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
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                                                                                                                                                                                                                                              240
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tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
                                                                                                                                                                                                                                                                              TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297
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                                                                                                                                                                         TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA
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                                                                               Score 284.2; DB 7; Length 496;
Pred. No. 1.9e-66;
0; Mismatches 8; Indels 0
                                                         Sequence 496 BP; 200 A; 95 C; 104 G; 95 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding human PRO polypeptide #267.
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                                                                             Query Match
Best Local Similarity 97.3%;
Matches 289; Conservative
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating bioactive molecules to cells expressing PRO polypeptides, for modulating contributions of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides are useful for contributing the release of tumour necrosis factor (TMP)-alpha from thuman blood, for stimulating the presence of tumours. The polymelectide chondrocytes, and detecting the presence of tumours. The polymelectide contribution of an incompanient of the proparation of PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and Companient of the preparation of PRO polypeptides, for generating transgenic conting the human PRO polypeptides for the secretaring transgenic content of an incompanient of the condaint properties of the invention. Note: The sequence content of the preparation of the invention. Note: The sequence content of the properties of the invention of the preparation of the intently from the preparation of the invention of the preparation of the intently from the preparation of the invention of the preparation of the intently from the preparation of the invention of the preparation of the preparation of the intently from the preparation of the invention of the preparation of the prepa
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ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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21-JUN-2001; 2001US-00887879.
22-JUN-2001; 2001MO-US02116.
29-JUN-2001; 2001MO-US021066.
09-JUL-2001; 2001WO-US021735.
18-JUL-2001; 2001US-00908827.
06-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-00927796.
16-AUG-2001; 2001US-00921836.
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//cgn2_6/ptodata/2/ina/RECTMS.comB.seq:*
//cgn2_6/ptodata/2/ina/PcTMS.comB.seq:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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US-08-888-497-28
US-09-362-230-28
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US-09-362-230-25
                                                                                                                                  682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                              nucleic search, using sw model
                                                                                                                  Gapop 10.0 , Gapext 1.0
                                                                                                                                                                length: 0
length: 2000000000
                                                                            US-09-830-321A-4
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Match Length DB
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                                                                                                                                                                Minimum DB
Maximum DB
                                                                                            Sequence:
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Sequence 28, Appl		Segmence 3. Appli	2.		i c	ī	ì ,-	1 6	, כי בי היים בי	1000	, ,	Semience 342, App	245,				Sequence 17202. A	Sequence 16656, A
PCT-US94-07926-28	US-08-809-763-3	US-08-956-253-3	US-09-621-976-15639	US-08-928-361B-2	US-09-588-995A-2	US-08-928-361B-1	US-09-588-995A-1	US-09-620-312D-330	US-09-620-312D-353	US-09-216-393B-340	US-09-216-393B-342	US-09-216-393B-343	US-09-216-393B-345	US-09-252-991A-7521	TIS - 03 - 230 - 225	110 00 CD1 CDC CDD-T	ns-na-ezT-a./e-1./202	US-09-621-976-16656
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6.5	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.0	6.0	0.9	0.9	0.9	6.0	5.0	6		0.	8. 8.
38.2	36.8	36.8	36.6	36.6	36.6	36.6	36.6	35.6	35.6	35.4	35.4	35.4	35.4	35.2	34.8	3.4.6	D .	34.4
28	53	30	c 31	32	33	34	35	c 36	c 37	38	39	40	c 41	42	43	44	# :	45

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
APPLICANT: Shyjan, Andrew W.
APPLICANT: Shyjan, Andrew W.
APPLICANT: Shyjan, Andrew W.
APPLICANT: Shyjan, Andrew W.
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER FILE REPERENCE: 07334-07401
CURRENT APPLICATION NUMBER: US 60/079,303
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 AGGAACCCCCAAGGATGGCACCGATTGGTGCTGTTGGGCGCATGACCACTGCTATGGGCG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 CCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 GAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467
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                      Sequence 17, Application US/09220132
Patent No. 6506607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.0
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-220-132-17
                                                                                                                                                                                                                                                                                                            NUMBER SOFTWARE: FAST:
SEQ ID NO 17
US-09-220-132-17
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Sequences and Low Molecular Weight Amino Acid Sequences Encoded Thereby, Antisense Sequences and Nucleotide Sequences Having Internal Ribosome Binding Sites
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                                        247 CCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGG 306
                                                                                 349 GCTGGAGGAGAAGACTGCAACATTCGCACAGTCCTACAATACAGATTCGCGTGGGG 408
289 AGGAACCCCCAAGGATGGCACCGATTGGTGCTGTTGGGCGCATGACCACTGCTATGGGCG 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Ami
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences a
TITLE OF INVENTION: Sequences Having Internal Ribosome Bir
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruden, Barnett, McClosky, Smith, Schuster
Russell PA
                                                                                                                                                                                                                                                                                                               427 CTGGCGGCCCCACTGCCGGGGCAGACCCCTGGGTGCT 464
                                                                                                                                                                                                                                                                                                                                                        526 TCCCAACATCTTGCTCCTAGGCCTCCCCAGCGAGCT 563
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
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APPLICATION NUMBER: 08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/09362230 Patent No. 6352849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1014 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: APPLICATION NUMBER:
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ADDRESSEE:
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US-09-362-230-31
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                                                                                                                                                                                Sequence 31, Application US/08888497

Batent No. 5972677

GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Becomed Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 IGGGAAAAIGCCCAICCICCIACIGGCCCIACGGCIGICACIGCGGACIAGGIGCAAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGCCAACCCAAAGATGCCACGGACTGCTGCCAGACCCATGACTGCTATGACCA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 TGGTGTGTTCCAATCCAGGGGGTCCTGAACCTGAACAAGATGGTCAAGTGAC 126
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llarity 57.8%; Pred. No. 2.8e-23;
Conservative 0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
                                                                                   528 receaacarécréréérecraégeerécéaédagér 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
                                             427 CIGGCGGCCCCACIGCCGGGGCAGACCCCTGGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN21044-5
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APPLICATION NUMBER: US/08/651,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/097,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN210
TELECOMMUNICATION INFORMATION:
TELEFAX: 305-764-4996
NFORMATION FOP CF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1014 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA APPLICATION NUMBER: UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Manso, Peter J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131..544
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Les 230; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-888-497-31
                                                                                                                                                            RESULT 2
US-08-888-497-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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3: Cushman, Darby 6
1615 L Street, N.W.
                                                                                                                                                                                       Query Match
Best Local Similarity 57.8%;
Matches 230; Conservative
            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-2601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                 131..544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hollis,
                                                                                                          , NAME/KEY:
, LOCATION:
PCT-US94-07926-31
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GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                              1,
                                                                    126
                                                                                                        228
                                                                                                                                               186
                                                                                                                                                                       229 AddgaAdaAcGccciGACAAACTACGGCTTCTACGGCTGTTACTGCGGCTGGGGCGGCCG 288
                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                            247 CCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGG 306
                                                                                                                                                                                                                                                                                                                            349 GCTGGAGGAGGAGGGCTGCAACATTCGCACAGTCCTACAAATACAGATTCGCGTGGGG 408
                                                                                                                                                                                                                                                                                                                                                                   307 GAACAICCACIGCICTGACAAGGGAAGCIGGIGIGAGCAGCAGCIGIGIGCCIGIGACAA 366
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                                                                                            169 radrichecrecrefichadeadecrrecresachanarcaardarcadeadedread
                                                                                                                                                                                                             187 AGGCCAACCCAAAGAIGCCACGGACTGGIGCIGCCAGACCCATGACTGGTGGTAIGACCA
                                                        127 IGGGAAAAIGCCCAICCICTCCIACIGGCCCIACGCCIGICACIGCGGACIAGGIGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 GAAGCTCGTCTACTGCCTCAAGAGAAACCTACGGAGCTACAAACCCACAGATACCTT
                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
    Pred. No. 2.8e-23;
0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 CTGGCGCCCCACTGCCGGGGGCAGACCCCTGGGTGCT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526 receaacarécrérdérecradecerécédadedr 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Manso, Peter J. REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, v. CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 base pairs
    57.8%;
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 33301
COMPUTER READABLE FORM:
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 GAAGCTCGTCTACTGCCTCAAGAGAAACCTACGGAGCTACAACCCACAGTACCTT 525
                                                                                                                                                                                                                 127 TGGGAAAATGCCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG
                                                                                                                                                                                                                                                                     229 AddeAAGAACGCCCTGACAACTACGGCTTCTACGGCTGTTACTGCGGCTGGGCCGCCG
                                                                                                       67 IGGIGIGATICCAATCCAGGGGGGGAICCTGAACCTGAACAAGATGGICAAGCAAGTGAC
                                                                                                                                                           169 TAGTGTGCCTGCTGCAAGGAGGCTTGCTGGACCTAAAATCAATGATGATGAAGGTGAC
                                                                                                                                                                                                                                                                                                                            187 AGGCCAACCCAAAGAIGCCACGGACTGGIGCTGCCAGACCCAIGACTGCTAIGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                      247 CCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 GAACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCTGTGTGCCTGTGACAA
                                                               Gaps
                                                            3;
Score 118; DB 5; Length 1014; Pred. No. 2.8e-23; 0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 CTGGCGGCCCCACTGCCGGGGCAGACCCCTGGGTGCT 464
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,895
FILING DATE: 27-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hollis, Melvyn
APPLICANT: Needham, Maurice R.C.
APPLICANT: Gooding, Clare
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: Expression Systems
NUMBER OF SEQUENCES: 10
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/046,383
FILING DATE: 09-APR-1993
APPLICATION NUMBER: US/07/810,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5538885
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGTTGACCACCTGAAGACCCAGG 260
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                        Length 479;
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                                                                                                                                                                                                                                                                                                                                                                                            19.0%; Score 112.4; DB 1; 54.4%; Pred. No. 7.6e-22; iive 0; Mismatches 206;
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                            NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stilhamer
TITLE OF INVENTION: EXPRESSION
ITILE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTIF PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
        ATTORNEY/AGENT INFORMATION:
                                                                                                                          TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    LENGTH: 479 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 249; Conservative
                                                                                                                                                                                                                                              single
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24..455
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                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                              TOPOLOGY: 11
MOLECULE TYPE:
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US-09-023-655-1207
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; LOCATION:
US-08-186-895-9
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Best Local
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141 TCCTCCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGGGCCAACCCAAAG 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 110.8; DB 4; Length 854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                  COMPUTER: IN POST ALLO COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS G.2 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS G.2 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/023,655 FILING DATE: HEREWITH CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGGGGGCAGACCCCTGGGTGCTAGAAGCCCACACCC 478
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2,6e-21;
2,6e-21;
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                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERBENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
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54.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 854 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 248; Conservative
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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CLONE: 9190888
US-09-023-655-1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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US-09-740-569-1
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Sequence 29, Application US/09362230

Patent No. 6352849

GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences and Low Molecular Meight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 IGAAGACCCAGGGGIGCGGCAICTACAAGGACTATTACAGATACAACTITTCCCAGGGGA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 ACATCCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCTGTGTGCTGCTGTGACAAGG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 GGAAAATGCCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGAACTAGGTGGCAGAG
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                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 AGGIGGCCTICIGCCIGAAGCGCAACCIGGACACCIACCA
                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
                                                                                                                                                                                                                             FILING DATE:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              32,264
                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: INTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 29:
               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1828 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   NAME: Manso, Peter J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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233..643
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MOLECULE TYPE: CDNA
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             MEDIUM TYPE:
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Best Local Simil
Matches 196; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
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                               APPLICANT: Weiss, Jerrold
APPLICANT: Weiss, Jerrold
APPLICANT: Elsbach, Peter
APPLICANT: Liang, Ning-Sheng
TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
FILE REPERENCE: 5986/18917031
CURRENT APPLICATION NUMBER: US/09/740, 569
PRIOR APPLICANTON NUMBER: US 60/172, 467
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5
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APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Ruseell PA
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Patent No. 5972677
GENERAL INFORMATION:
                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 56.6
Matches 209; Conservative
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                    GENERAL INFORMATION:
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LENGIH: 375
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Patent No.
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APPLICANT: Tischfield, Jay A. APPLICANT: Tischfield, Jay A. APPLICANT: Seilhamer, Jeffrey J. TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide TITLE OF INVENTION: Sequences and Low Nolecular Weight Amino Acid Sequences TITLE OF INVENTION: Sequences and Low Nolecular Weight Amino Acid Sequences TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS: ADDRESSE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA

STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACATCCACTGCTCTGACAAGGGAAGGTGGTGAGAGCAGCAGCTGTGTGACAAGG 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 GGRAAATGCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAG 188
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16.6%; Score 98.4; DB 5; Length 1828;
Best Local Similarity 57.6%; Pred. No. 9e-18;
Matches 196; Conservative 0; Mismatches 141; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 AGGIGGCCTTCTGCCTGAAGCGCAACCTGGACACCTACCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patenth Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926 FILING DATE: 15-JUL-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 29
SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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    GENERAL INFORMATION:
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, LOCATION:
PCT-US94-07926-29
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                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 GGAAAATGCCCCATCCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAG 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAICCACTGCTCTGACAAGGGAAGCTGGTGTGAGCAGCAGCAGCTGTGTGTCTGACAAGG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 dehaghangceghangnachangernethedechechenkengergedegedeched
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.6%; Score 98.4; DB 4; Length 1 Best Local Similarity 57.6%; Pred. No. 9e-18; Matches 196; Conservative 0; Mismatches 141; Indels
                             ADDRESSEB: Ruden, Barnett, McClosky, Smith, Schuster ADDRESSEB: Russell PA STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570 Agcregarcracrecordagadaaaccregagaracaa 609
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                                                                                                                                                                                                                         SOFTWARE: Patentin RC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/362,230 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IN21044-5
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PCT-US94-07926-29
; Sequence 29, Application PC/TUS9407926
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 08/097,354
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-JUL-1993
ATTORNAY AGENT INFORMATION:
NAME: MANSO, PECET J.
REGISTRATION NUMBER: 32,264
REFERSINCE/DOCKET NUMBER: IN21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233..643
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                                                                                                                                                    USA
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US-09-362-230-29
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                                                                                                                                                    COUNTRY:
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                                                                                                         CITY: F
STATE:
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Sequence 21, Application US/09362230
Ratent No. 6152849
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nuclectide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
           975 ATGGCTGCCAGCCATCTTGAATGCCTATCAGTTTGCCATTGTCAACGGGACCGTGACCT 1034
                                                                                                                    1035 GTGGATGCACCATGGGGGGGGGCTGCTTGTGCGGGCAGAAAGCCTGTGAGTGTGAGAAC 1094
                                                                           318 G------CTCTGACAAGGGAAGCTGGTGTGAGCAGCTGTGTGTGCCTGTGACAAGG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      795 ccacccrcadcagerricrescaerreccadadardercaaacacarcaces
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                                                                                                                                                                                                  1095 TGTCTGTGTACTGCTTCAAGGAGAAACCTGGCCACCTACGAGAA 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster
ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                              369 AGGIGGUCTICIGCCIGAAGCGCAACCIGGACACCIACCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 92.6; DB 4;
Pred. No. 4.9e-16;
0; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Broward Boulevard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: US 08/097, FILING DATE: 26-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.6%;
56.9%;
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Best Local Similarity 56.9
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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722..1195
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                                                                                                                                                                                                                                                                RESULT 12
US-09-362-230-21
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LOCATION:

US-09-362-230-21
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                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Silhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATCCTCTCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGGCCAACCCA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccricricricitàriacgararadecrecracidresecrireseseceasesearecere 914
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llarity 56.9%; Pred. No. 4.9e-16;
Conservative 0; Mismatches 139; Indels 9
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA STREET: 200 East Broward Boulevard CITY: Fort Lauderdale
570 AGCTGGTCTACTGCCTGAGGAGAACCTCTGGAGTTACAA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN21044-5
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APPLICATION NUMBER: US/08/651,405
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                                                                                                    Sequence 21, Application US/08888497
Patent No. 5972677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: INTELECOMMUNICATION: 1NFORMATION:
TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08
FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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722..1195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33301
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; LOCATION:
US-08-888-497-21
                                                                                JS-08-888-497-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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Best Local S:
Matches 195,
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                                                    138 CCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGGCCAACCCA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 139;
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TELEPHONE: 650-855-0555
TELEFAX.
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08966317
Patent No. 6103469
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 742 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
      Conservative
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IMMEDIATE SOURCE:
LIBRARY: OVARTU
CLONE: 816403
         Matches 195;
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APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
TITLE OF INVENTION: McClosky, Smith, Schuster & ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
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Pred. No. 4.9e-16;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: PCT/US94/07926
15-JUL-1994
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APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US94-07926-21; Sequence 21, Application PC/TUS9407926; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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56.9%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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Best Local Similarity
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Search completed: October 7, 2004, 18:59:22
Job time : 49.7926 secs
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                                    Score 63.2; DB 3; Length 742;
Pred. No. 3.5e-08;
0; Mismatches 133; Indels
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APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
ITILE OF INFUTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                          378 TCTGCCTGAAGCGCAACCTGGACACCTACCAGAAGC 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,770
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/966,317
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0403
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09489770
Patent No. 6399301
                                  Best Local Similarity 51.8%;
Matches 143; Conservative (
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SEQUENCE CHARACTERISTICS:
LENGTH: 742 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: OVARTUT01
CLONE: 816403
                                Query Match
Best Local Similarity
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US-08-966-317-2
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STATE:
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                                                             Gaps
                                                             0
        Length 742;
Score 63.2; DB 4; Length 7:
Pred. No. 3.5e-08;
0; Mismatches 133; Indels
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  Query Match
Best Local Similarity 51.8%;
Matches 143; Conservative
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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

7, 2004, 16:44:09; Search time 303.834 Seconds (without alignments) 9877.707 Million cell updates/sec October Run on:

US-09-830-321A-4 592 Title: Perfect score:

1 tetgeeteeaetgetetgtg.......seeageeteeeeggaaeee 592 Scoring table: Sequence:

3340653 segs, 2534783454 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Published Applications NA:*

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| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 5, Appli Sequence 377, App Sequence 377, App Sequence 533, App Sequence 533, App Sequence 533, App Sequence 533, App Sequence 533, App Sequence 533, App Sequence 533, App Sequence 533, App Sequence 533, App Sequence 533, App Sequence 6, Appli Sequence 603, Ap Description US-09-835-996A-5 US-09-946-374-377 US-10-147-493-533 US-10-145-127-533 US-10-143-118-533 US-10-144-993-533 US-10-144-993-533 US-10-144-993-533 US-10-146-993-533 US-10-146-808-533 US-10-140-808-533 US-10-296-115-603 US-09-969-384-6 SUMMARIES DB Query Match Length 996.1 995.8 448.0 448.0 448.0 448.0 448.0 448.0 448.0 448.0 2567.4 2084.2 2084.2 2084.2 2084.2 2084.2 2084.2 2084.2 2084.2 2084.2 Score 575. Result

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ALIGNMENTS

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| CENTERAL INFORMATION: Human Gene Polynucleotides, Polypeptides, and Antibodies |
| TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies |
| FILE REFRENCE: PFOSEPI |
| CURRENT APPLICATION NUMBER: US/09/969,384 |
| CURRENT APPLICATION NUMBER: D01-10-03 |
| PRIOR APPLICATION NUMBER: PCT/US01/10542 |
| PRIOR PILING DATE: 2001-04-02 |
| PRIOR FILING DATE: 2000-09-29 |
| PRIOR FILING DATE: 2000-09-29 |
| PRIOR FILING DATE: 2000-04-03 |
| NUMBER OF SEQ ID NOS: 27 |
| SOFTWARE: PatentIn Ver. 2.0 |
| SEQ ID NO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO SECONO S
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                                                Sequence 6, Application US/09969384 Publication No. US20020192749A1 GENERAL INFORMATION:
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Best Local Similarity
Watches 576; Conserv
US-09-969-384-6
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APPLICANT: Zhao, Qing
APPLICANT: ABURILL, ALLOAD
APPLICANT: Wehrman, Tom
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Kadoje
APPLICANT: Ren, Kadong
APPLICANT: Qian, Kiahong
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APPLICANTON NUMBER: US 09/114,336
PRIOR PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
SEQ ID NO 5
                                 GCCCCACTGCCGGGGGAGCCCCTGGGTGCTAGAAGCCCAACACCCTCTACCCTGTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.8%; Score 567.4; DB 9;
99.8%; Pred. No. 3.8e-168;
iive 0; Mismatches 1;
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Tang, Y. Tom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
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Matches 568; Conservative
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ORGANISM: Homo sapiens
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APPLICANT:
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                                                                                                                                      CANAGATGCCACGGACTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAAGAC 248
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        CTTCTGCCTGAAGGGAACCTGGACACCTACCAGAAGGGACTGCGTTTCTACTGGCGGCC
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Pred. No. 1.4e-168;
0; Mismatches 7;
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al Similarity 98.8%;
573; Conservative 0
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Best Local Similarity
Matches 573; Conserv
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US-10-296-115-603
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                                                                                                                                                                                                                                                                                                                             GCGGCATCTACAAGGACTATTACAGATACAACTTTTCCCAGGGGAACATCCACTGCTCTG 323
                                                                                                                                                                                           13 AGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGCCCATCC 132
                                                                                    AGGCCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGACTGGGAAAATGCCCATCC 143
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
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                           13 GGACCATGGAACTTGCACTGCTGTGGGCTGGTGGTGATGGCTGGTGATTCCAATCC
      GGATCATGGAACTTGCACTGCTGTGGGCTGGTGATGGCTGGTGATTCCAATCC
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CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Publication No. US20030073129A1
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Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
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FILING DATE: 1998-09-17
APPLICATION NUMBER: 60/101014
FILING DATE: 1998-09-18
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FILING DATE: 1998-09-15
APPLICATION NUMBER: 60/100388
ELING DATE: 1998-09-15
APPLICATION NUMBER: 60/100390
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APPLICATION NUMBER: 60/100584
FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100627
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APPLICATION NUMBER: 60/100683
FILING DATE: 1998-09-17
APPLICATION NUMBER: 60/100684
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APPLICATION NUMBER: 60/100710
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APPLICATION NUMBER: 60/100711
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APPLICATION NUMBER: 60/100848
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APPLICATION NUMBER: 60/100849
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APPLICATION NUMBER: 60/099816
FILING DATE: 1998-09-10
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099754
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APPLICATION NUMBER: 60/099808
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FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099596
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APPLICATION NUMBER: 60/099602
APPLICATE: 1998-09-09
APPLICATION NUMBER: 60/099642
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APPLICATION NUMBER: 60/099792
                                                             APPLICATION NUMBER: 60/098750
FILING DATE: 1998-09-01
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FILING DATE: 1998-09-02
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APPLICATION NUMBER: 60/098843
FILING DATE: 1998-09-02
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60/098723
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                  FILING DATE: 1998-09-01
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PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: 60/10171

PRIOR PRIOR PLING DATE: 1998-09-22

PRIOR APPLICATION NUMBER: 60/101471

PRIOR PELING DATE: 1998-09-23

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GATGGCTGGTGTGATTCCAATCCAGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120 61 GATGGCTGGTGATTCCAATCCAGGGGGATCCTGAACCTGAACAAGATGGTCAAGGA 120 240 121 AGTGACTGGGAAAATGCCCATCCTCTCTACTGGCCCTACGGCTGTCACTGCGGACTAGG 180 9 TGACCACCTGAAGACCCAGGGGTGCGGCATCTACAAGGACTATTACAGATACAACTT 297 1 TCTGCCTCCACTGCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGGGCTGGTGGT TGGCAGAGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTA APPLICANT: Faoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830PlC57
CURRENT APPLICATION NUMBER: US/10/015,395A ., DB 10; Length 496; Indels .2; 4.4e-79; Query Match
Best Local Similarity 97.3%; Pred. No. 4.4e
Matches 289; Conservative 0; Mismatches PRIOR FLLING JAILS: 1938-10-08
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
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PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-14
PRIOR PLING DATE: 1998-10-14
PRIOR PRING DATE: 1998-10-14
PRIOR PRING DATE: 1998-10-20
PRIOR PLING DATE: 1998-10-20
PRIOR PLING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/10500
PRIOR APPLICATION NUMBER: 60/10500
PRIOR PLING DATE: 1998-10-20
PRIOR PLING DATE: 1998-10-20
PRIOR PLING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR PLING DATE: 1998-10-22
PRIOR PLING DATE: 1998-10-22
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C345
CURRENT APPLICATION NUMBER: US/10/147,493
CURRENT FILING DATE: 2002-05-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
LENGTH: 496
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                Prior application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 377
LENGTH: 496
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Pred. No. 4.4e-79;
0; Mismatches 8;
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Publication No. US20040029217A1
GENERAL INFORMATION:
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CTHER INFORMATION: unknown base
US-10-015-395A-377
  2001-12-12
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 97.3%;
Matches 289; Conservative
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Tumas, Daniel
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Smith, Victoria
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                                                                                             TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
CURRENT FILING DATE:
                                                                                                                                                         NAME/KEY: unsure
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330NCCE: P3350NCCE: P3350NCCE: P3350NCCE: P3350NCCE: P3350NCCE: P3350NCCE: P3350NCCE: P3350NCCE: P3350NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE: P3550NCCE
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NUMBER OF SEQ 1D NOS: 550
                                                                                                                                                                DB 13;
                                                                                                                                                        Score 284.2; DB 13;
Pred. No. 4.4e-79;
0; Mismatches 8;
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48.0%; Score 284.2; DB 1.
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8
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Publication No. US20040033558A1
                                                                                                                                                        Query Match
Best Local Similarity 97.3%; Pre
Matches 289; Conservative 0;
; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-147-493-533
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Stewart, Timothy A
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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APPLICANT: Beresini, Maureen
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Wood, William
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                                          241 IGACCACCIGAAGACCCAGGGGIGCGGCAICIACAAGGACIAIIACAGAIACAACII 297
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCENETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C228
                 TGGCAGAGGCCAACCCAAAGATGCCACGGACTGCTGCCAGACCCATGACTGCTGCTA
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CURRENT FILING DATE: 2002-05-09
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                                                                                                             Sequence 533, Application US/10143118
Publication No. US20040038335A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: unknown base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen, Mary E
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Filvaroff, Ellen
Gao, Wei-Qiang
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Gurney, Austin L.
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Matches 289; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goddard, Audrey
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                      RESULT 9
US-10-143-118-533
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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C446
CURRENT APPLICATION NUMBER: US/10/160,503
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 533
LENGTH: 496
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Score 284.2; DB 13; Length 496;
Pred. No. 4.4e-79;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 533, Application US/10160503 Publication No. US20040033559A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: 396
; OTHER INFORMATION: unknown base
US-10-160-503-533
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Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
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Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity
Matches 289; Conserv
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US-10-160-503-533
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 533
LENGTH: 496
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Pred. No. 4.4e-79;
0; Mismatches 8;
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Publication No. US20040039164A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                     Application US/10144993
o. US20040038336A1
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LOCATION: 396

US-10-144-993-533
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Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
US-10-144-993-533
; Sequence 533, Application US/103; Publication No. US20040038336A1; Publicate NFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
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Best Local Similarity 97.3%;
Matches 289; Conservative
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Filvaroff, Ellen
Gao, Wei-Qiang
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Godowski, Paul J
Gurney, Austin L.
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ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P0330R16449

CURRENT PILION DATE: 2003-04-03

PRIOR PELICATION NUMBER: 60/06911

PRIOR PILING DATE: 1997-06-18

PRIOR PELICATION NUMBER: 60/069113

PRIOR PELICATION NUMBER: 60/069113

PRIOR PELICATION NUMBER: 60/069115

PRIOR PELICATION NUMBER: 60/069117

PRIOR PELICATION NUMBER: 60/069117

PRIOR APPLICATION NUMBER: 60/069117

PRIOR APPLICATION NUMBER: 60/069117

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 396
COTHER INFORMATION: unknown base
US-10-158-787-533
                                                                                                                                                                                                                                                    Stewart, Timothy A
                                                                  Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                   Watanabe, Colin K
Wood, William
                                                                                         Goddard, Audreý
Godowski, Paul J.
Gurney, Austin L.
Filvaroff, Ellen
Gao, Wei-Qiang
                                                                                                                                                                                            Sherwood, Steven
Smith, Victoria
                                                                                                                                                                                                                                                                                        Tumas, Daniel
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 289; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: unsure
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GATGGCTGGTGTGTTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 284.2; DB 13; Length Pred. No. 4.4e-79; 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan J.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 377, Application US/10006485A Publication No. US20030064062A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; CTHER INFORMATION: unknown base US-10-140-808-533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.3%;
Matches 289; Conservative
                                                                                                                                                                   Smith, Victoria
Stewart, Timothy A.
                                                                                                Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                  Gerritsen, Mary E
                                  Desnoyers, Luc
Filvaroff, Ellen
                                                                  Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
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US-10-006-485A-377
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APPLICANT:
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APPLICANT:
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241 TGACCACCTGAAGACCCAGGGTGCGGCATCTACAAGGACAACAACAAAAAGCAGCAT 297
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1998-09-18

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FILING DATE: 1998-10-02
APPLICATION NUMBER: 60/103258
FILING DATE: 1998-10-06
                                                                        FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/100919
FILING DATE: 1998-09-17
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FILING DATE: 1998-09-17
APPLICATION NUMBER: 60/101014
FILING DATE: 1998-09-18
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ILING DATE: 1998-09-23
PPLICATION NUMBER: 60/101738
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APPLICATION NUMBER: 60/103315
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FILING DATE: 1998-10-07
APPLICATION NUMBER: 60/103395
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FILING DATE: 1998-09-22
APPLICATION NUMBER: 60/101471
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APPLICATION NUMBER: 60/101472
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ILING DATE: 1998-09-23
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ILING DATE: 1998-09-23
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ILING DATE: 1998-09-23
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FILING DATE: 1998-09-23
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ILING DATE: 1998-09-24
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ILING DATE: 1998-09-24
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TLING DATE: 1998-09-24
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ILING DATE: 1998-09-29
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FILING DATE: 1998-09-29
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FILING DATE: 1998-09-29
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FILING DATE: 1998-09-30
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FILING DATE: 1998-09-30
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FILING DATE: 1998-09-30
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FILING DATE: 1998-10-01
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FILING DATE: 1998-10-02
                                                  APPLICATION NUMBER: 60/100849
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/101068
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PPLICATION NUMBER: 60/101741
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                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/101071
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PRIOR
             APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPREBREE: P2830PLC9
CURRENT APPLICATION NUMBER: US/10/006,485A
CURRENT FILING DATE: 1098-109-01
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR FILING DATE: 1998-09-01
PRIOR FILING DATE: 1998-09-01
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R FILING DATE: 1998-09-01
R APPLICATION NUMBER: 60/098750
R FILING DATE: 1998-09-01
R APPLICATION NUMBER: 60/098803
R FILING DATE: 1998-09-02
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APPLICATION NUMBER: 60/099598
RILING DATE: 1998-09-09
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FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100662
FILING DATE: 1998-09-16
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APPLICATION NUMBER: 60/100710
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APPLICATION NUMBER: 60/100711
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FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099741
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099808
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FILING DATE: 1998-09-15
APPLICATION NUMBER: 60/100390
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FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100627
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APPLICATION NUMBER: 60/099596
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FILING DATE: 1998-09-10
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FILING DATE: 1998-09-10
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FILING DATE: 1998-09-15
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FILING DATE: 1998-09-17
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FILING DATE: 1998-09-02
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Gurney, Austin L.
Hillan, Kenneth J.
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61 GATGGCTGGTGTGATTCCAATCCAGGGGGATCCTGAACTGAACAAGAAGATGGTCAAGCA 120
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48.0%; Score 284.2; DB 13;
Best Local Similarity 97.3%; Pred. No. 4.4e-79;
Matches 289; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                              APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pani, Nicholas F.
APPLICANT: Pani, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembran
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC34
CURRENT APPLICATION NUMBER: US/10/013,907A
CURRENT FILING DATE: 2001-12-10
                                                                                                                                                             Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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                                            Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Desnoyers, Luc
Eaton, Dan 1.
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ORGANISM: Homo sapiens
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LOCATION: 396
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                                                                                                     APPLICATION NUMBER: 60/103449
FILING DATE: 1998-10-06
APPLICATION NUMBER: 60/103633
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FILING DATE: 1998-10-20
APPLICATION NUMBER: 60/105002
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APPLICATION NUMBER: 60/105104
FILING DATE: 1998-10-21
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FILING DATE: 1998-10-22
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FILING DATE: 1998-10-22
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FILING DATE: 1998-10-26
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APPLICATION NUMBER: 60/103678
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APPLICATION NUMBER: 60/103679
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FILING DATE: 1998-10-14
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FILING DATE: 1998-10-26
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APPLICATION NUMBER: 60/106023
                                               APPLICATION NUMBER: 60/103401
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APPLICATION NUMBER: 60/103711
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Matches 289; Conserv
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Sequence 377, Application US/10013907A Publication No. US2003064925A1 GENERAL INFORMATION: APPLICANT: Baker, Kevin P.

RESULT 15 US-10-013-907A-377

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nucleic search, using sw model OM nucleic 7, 2004, 11:14:15; Search time 937.252 Seconds (without alignments) 9989.875 Million cell updates/sec October Run on:

US-09-830-321A-5 2204 Title: Perfect score:

IDENTITY NUC Scoring table: Sequence:

3373863 seqs, 2124099041 residues Searched:

Gapop 10.0 , Gapext 1.0

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

N Geneseq_29Jan04:*

1: geneseqn1980s:*
2: geneseqn1980s:*
3: geneseqn2001s:*
5: geneseqn2001as:*
5: geneseqn2001as:*
7: geneseqn2001as:*
7: geneseqn2003as:*
8: geneseqn2003as:* geneseqn2003cs:* geneseqn2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	0 Aaa53270 Human pho	7 Aaz88757 Human PLA			0		8 Aaf90488 Human pho	3 Aas17363 cDNA enco	4 Abx11884 Human cDN	2 Aas17362 Partial C		Aav34229	0 Acd08100 cDNA enco	4 Aav34164 Human sec		Aav34230	1 Acd08101 cDNA enco	1 Aas84341 DNA encod	6 Aaz88756 Human PLA	8 Aaf74998 Phospholi		8 Aas70058 DNA encod	6 Aas70056 DNA encod
ΩĦ	AAA5327	AAZ8875	AAZ88758	AAF74999	AAF7500	AAF90489	AAF90488	AAS17363	ABX11884	AAS17362	ABX11883	AAV34229	ACD08100	AAV34164	ACD08035	AAV34230	ACD08103	AAS8434	AAZ88756	AAF74998	AAF90487	AAS70058	AAS70056
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Score	2202	1816.8	1816.8	1816.8	1816.8	1816.8	1816.8	1806.2	1806.2	1806.2	1806.2	1788.8	1788.8	1777.8	1777.8	1676.6	1676.6	1432.2	1408.6	1408.6	1408.6	1388.8	728.8
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ALIGNMENTS

Human, phospholipase 2; HPPL2; cancer, autoimmune disorder; inflammatory disorder; reproductive disorder; infection; ss. Human phospholipase 2 HPPL2 coding sequence. AAA53270 standard; cDNA; 2204 BP 05-OCT-2000 (first entry) AAA53270; RESULT 1 AAA53270

Location/Qualifiers 95. .1912 /*tag= a Homo sapiens.

/*tag= a /product= "HPPL2" WO200024911-A2 04-MAY-2000

99WO-US025021. 27-OCT-1999;

98US-00181317. 99US-00234726. (INCY-) INCYTE PHARM INC. 27-OCT-1998; 21-JAN-1999;

Baughn MR; Hillman JL, Bandman O, Guegler KJ, Corley NC, Azimzai Y, Lal P, Lu DAM; WPI; 2000-350750/30. P-PSDB, AAB03628

Human phospholipase genes and proteins useful to diagnose, prevent or treat cancer, autoimmune or inflammatory or reproductive disorders. Claim 9; Page 74-75; 80pp; English.

The present sequence is the coding sequence of human phospholipase 2 (HPPL2). The protein produced from this sequence is involved in the hydrolysis of membrane phospholipids. The protein and its coding sequence can be used to diagnose and treat the following: cancers such as

1080 1440 1020 1200 1200 1260 1320 1320 1380 1440 1500 1560 1560 1620 1620 CTCGGGAGTGCCACACTTCTCCGACCCCACTGCCCGGAGCCCCTGC 1680 1740 1740 1860 1860 GCCAGGCAGTGCAGCGGAGGCGCAGCGCAGGCCCCACTGATGGCCGGG 1920 AAGCTCTCAGAICAACGGGGGGCCCTGAGTCAIGGCCAGAACCCTCTGCC 900 SCCTCAACACCAAAGGGCAGACCTGACCACTTTTGAATTTGGGGAGTG 960 AAGGTATCTGGAGCAACTGTATGCAGCCAACCTCCAGGACAGCTTATA AGCCCAGCCAGTTCTGGGACCGCTGGGTCAGGAACCAGGCCAACCTGGA TCCCCCTTCTGAAGATAGAAGAACCCCCTCAACAGCCGGCAGAATAGC CCGATCTTCTGACGTGGCGTCCACTGGCCCAGGCCACACATAATTTCCT ATGGGCTCCCCAACCAGCTGACACCTCGGAGCCCCACCTGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCCCCACCTCGGACCCCCACCTGTGCCTGCT CCGAGTTCTTTATGGGGCAGCTGATGAAGAGGCTTCCTGAGTCCCGCAT ACCTCATCAATACCAGCTGCCTGCCCTCCTGCAGCCCACTCGGGACGT GCCAGGAGCAGGGATCCCGTTCCCACCCATCTCGCCCAGCCCCGAAGA ATTICCACAAAGACTACTTICAGCATCCTCACTTCTCCACATGGAAAGC TITCCTCTGGGGGTCCGGCGGACACCCGAGGAGGGGGCAGCTGGGGAGGT TGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCT TTTCCTCTGGGGTCCGGCGGACACCCGAGGAGGCGGCGGCAGCTGGGGAGGT PATCGGACTCTCCCTACCACTACACGAGGTGACCTACAGCCAGGAGGA

(also

phospholipase A2. This sequence encodes the human PLA2 protein known as phosphatide 2-acyl hydrolase)

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GCCCCTGCCACCCCTAACTCTCATTCATTCCCTGGCTGAGTTGCAGGTGGGAACTGT 1980
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          1921 GCCCTGCCACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGT
                                 CATCACGCAGTGCTTCAGAGCCTCGGGCTGAGGTGGCACTGTCCCAGGGTCCAGGCTGAG
                                             GGCTGGGAGCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGGTAAGGAGGCCAAGCCCATTT
                                                                              GTGTAATCACCCCAAAACCCCCCCCGGCCTGTGCTTTTCCCTTCTGCGCTACCTTGAGTA
                                                                                                                 PLA2; phospholipase A2; phosphatide 2-acyl hydrolase; human; therapy; arachidonic acid; lysophospholipid; Alzheimer's disease; ss.
                                                                                                                                        Kramer RM, Pickard
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This invention describes a novel human phospholipase A2 (PLA2) protein (I) and its encoding nucleic acid. The amino acid (I) releases arachidonic acid in specific tissues characterized by unique membrane phospholipids, by generating lysophospholipid species which are deleterious to membrane integrity or by remodeling of unsaturated species of membrane phospholipids through deacylation/reacylation mechanisms. The amino acid is useful in assays to identify inhibitors having a therapeutic benefit, such as inhibiting the central role of PLA2 in the inflammatory component of Alzheimer's disease. The amino acid (I) allows sensitive and rapid screening and identification of inhibitors of

Example 5; Col 47-54; 32pp; English.

1305 ij 1485 1365 1425 1545 1605 1665 1001 1061 401 461 1121 1965 2025 521 641 1181 1241 2085 2145 581 701 761 821 881 1242 CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 1301 342 GACTGAGGAGCTGGCGTGCGACTGGGCTTCGGGCCCTGTGCAGAGGAGCAGGCCTTCC ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGGGATCCGGG CAATGACTTCCCTGTATGGGCAGCTGGCTGGAAGGAGCTGGGCTCTTGGATTGCG 1366 CAATGACTTCCCTGTATGGGCAGCTGGCTGGCTGAAGGAGCTGGGGCCTCTTGGATTGCG 582 ICICCTACATCACGGGGCCTCGGGCTCCTGGGCCTTGGCCAACCTTATGAGGACC 1426 TCTCCTACATCACCGGGGCCTCGGGCTCCACCTGGGCCTTGGCGAACCTTTATGAGGACC 642 CAGAGTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGGTGAAGACCCAAGGTGACCA 1486 CAGAGTGGTCTCAGAAGGACCTGGCCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA 702 AGAACAAGCTGGGTGTGCTGGCCCCCCAGCTGCAGCGGTACCGGCAGGAGCTGGCCG 1606 AGCGTGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCCTCATCAACGAGG CGCTGCTGCATGATGAGCCCCCATGATCACACTCTCAGATCAACGGGAGGCCCTGAGTC 762 AGGGGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG 1846 GGGCCTTCATCCCCTCTGAGCTCTTTGGCTCCCAGTTCTTTATGGGGCAGCTGATGAAGA 1906 GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCAGTATGCAGCCA ATGGCCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAAGGCCAGAGCCTGACCA CTITIGAATTTGGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGCTTCCCCAAGTACG GGGCCTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA 1062 GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 1182 GGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCTTCTGAAGATAGAAGAACCACCCT Gaps 1966 ACTCCAGGACAGCTTATACTGGGCCTCAGAGCCCAGCTAGTTCTGGGACCGCTGGGTCA 2026 GGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCT 2086 CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 33; Length 3085; Sequence 3085 BP; 607 A; 959 C; 907 G; 612 T; 0 U; 0 Other; Indels DB 3; 5 82.4%; Scor. 98.2%; Pred. No. v, 98.2%; Pred. No. v, ... Matches 1861; Conservative Local Similarity 1186 402 462 522 Query Match 1666 882 1002 822 942 8 **%** 8 8 ठ 셤 ð qq ò d à g ò a 8 g ò g ર્જ D à qq à g à qq ð g du ð ð Db à 엄 ò d

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Pickard

Kramer RM,

Choiu XC,

Strifler BA,

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97US-00827208 96US-0014608P

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PLA2; phospholipase A2; phosphatide 2-acyl hydrolase; human; therapy; arachidonic acid; lysophospholipid; Alzheimer's disease; ss.
Human PLA2 mRNA
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                                       Homo sapiens
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(first entry)

18-MAY-2000

standard;

AAZ88758

RESULT 3 AAZ88758

AAZ88758

DXXXEX BXXXEX

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ខ្លួ 1665 1725 1785 1845 1001 1546 AGAACAAGCUGGGUGUGCCCCCCAGCCAGCUGCAGCGGUACCGGCAGGAGCUGGCCG 1605 1001 1905 1121 1965 2025 1241 2085 2145 1181 1301 1361 1421 2385 2445 TGCAGCCCACTCGGGACGTGGACCTCATCGTCATTGGACTACAACCTCCACGGAGCCT 1541 2505 1693 2325 TCTCGCCCAGCCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCA 1661 1808 881 941 821 CAACAGCGGGGAGAATAGCTGAGTTTTTCACCGATCTTCTGAGGTGGGGTCCACTGGCCC CTITIGAATITGGGGAGTGGTGCGAGTICTCTCTCTACGAGGTCGGCTTCCCCAAGIACG GGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCT CGCTGCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTC ATGGCCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAAGGGCAGAGCCTGACCA GGGCCTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGAAGA GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA ACCTCCAGGACAGCTTATACTGGGCCTCAGGCCCAGTTCTGGGACCGCTGGGTCA AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC ACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGACACCTCGG ----TCCTCTGGGGTCCGGCGGACACCCGAGGCGGCAGCTGGGGAGGTGAACCTGT ACUCAGCCCCUGGGGUCCGGCGGACACCCGAGGAGGCGGCAGCUGGGGAAGCUGGAACCUGU CTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGGACA CCTGCCCGGAGCCCCTGCGGTGCTGCACTTT------1606 1666 1726 1966 762 822 882 1786 1846 1062 1906 1122 942 1002 1182 2026 1242 2086 1302 2146 1362 2206 2266 2326 2386 1602 2446 1749 2626 1422 1482 1542 1662 2506 1694

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අු	2686	GACACAUVACAAUGUCUGCAACAACCAGGAGCAGCUGCUGGAGGCUC 2745
ð í	1869	TGCGCCAGGCAGTGCAGCGGAGCGGCAGCGCAGCTGATGGCCGGGGCCCTGC 1928
qq	2746	GCAGCGGAGCGGCAGGCCCCCACUGAUGGCCGGGGCCCCUGC 2805
ð í	1929	CACCCCTAACTCTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC 1988
qu	2806	CAUUCAUUCCCUGGCUGCUGAGUUGCAGGUGGGAACUGUCAUCACGC 2865
ð í	1989	04
an n	7866	CUCGGGCUCAGGUGGCACUGUCCCAGGGUCCAGGCUGAGGCCUGGGA 2925
රි සි	2049	GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAAGCCCATTTGTGTAATC 2108 : :: : :: : : GCUCCCUUGCGCCCCAGTUUGCAGUGGGGUAAGGAGGCCAAGCCCAUUUGUGUAAUC 2985
70	2109	216
qq	2986	caaccuauaccuauuucccuucuacacuuaaauauuaaaac 3045
ያ ሀ	2169	ACTTGATACATCACAGGCTCATACAAAAAAAAA 2204 : : :
EX.	RESULT 4	
₹A×9	AAF/4999 ID AAF/4999 standard; cDNA; AC AAF/4999;	A; 3085 BP.
XE	23-MAY-2001 (first	entry)
Z E Z	(3 Phospholipase A2 (PLA2)	encoding cDNA SEQ ID NO:2.
\$ & & \$	W Phospholipase A2; PLA2; Y rheumatoid arthritis; ps	; antiinflammatory; inflammatory condition; osoriasis; asthma; cytosolic PLA2; cpLA2; ss.
\$8\$	Homo sapiens.	÷
X & X	US6197569-B1.	,
E X	06-MAR-2001.	×20.0
PF	07-FEB-2000; 2000US	-00500358.
# # # # # # # # # # # # # # # # # # #	29-MAR-1996; 96US-0014608P. 19-MAR-1997; 97US-0041264P. 28-MAR-1997; 97US-00827208.	4608P. 11264P. 127208.
X & X	(ELIL) LILLY & CO ELI.	
M	Choiu XC, Kramer RM,	Pickard RT, Sharp JD, Strifler BA;
* # # \$	WPI; 2001-256372/26. P-PSDB; AAB74635.	
{	Novel nucleic aci screening assays phospholipase A2	d molecules encoding phospholipase A2 enzyme, useful in for identifying compounds that inhibit or block enzyme activity.
PS X	Claim 1; Col 47-54;	32pp; English.
8888		The present invention describes an isolated polymucleotide (I), Accomprising a 3085 base pair phospholipase A2 (PLA2) sequence (given in AAF74999), encoding a 913 residue phospholipase A2 protein sequence

(given in AAB74635), or a nucleotide sequence which hybridises un stringent conditions to the above mentioned nucleotide sequence.

2169 ACTTGATACATCACAGACTCATACAAAAAAAAAAAA 2204 2109 2986 2866 2386 2446 1662 2506 2566 1809 2686 1869 2746 1929 2806 1989 2049 1422 1482 2326 1542 1602 1694 1749 2206 2266 2626 1182 2086 1302 2146 1362 1122 1966 1242 qq d qq d ò g Š g à g à Ωp δ g à Dp à g ò g ð ð ò d 음 ò ð g g Qγ δ g P 24 ò ð described are: (1) an isolated polymucleotide (II) comprising an 8517 base pair sequence, given in AAF74998; (2) an expression vector (III) comprising (I) and an expression control sequence; (3) a host cell transformed with (III); (4) an expression vector (IV) comprising (II) operably linked to an expression control sequence; and (5) a host cell transformed with (IV). (I) is useful for screening compounds which inhibit or block cytosolic FLA2 (oFLA2) enzyme activity. The host cells transformed or transformed or transfected with cFLA2 enzymes in large quantities which are useful in screening assays for discovering agents that inhibit PLA2. The inhibitors identified are useful for treating inflammatory conditions such as rheumatoid arthritis, psoriasis, or asthma. (I) is also useful in the detection of mutant genomic DNA which has been digested with restriction enzymes and run on an electrophoretic gel by hybridising to the genomic DNA 1485 1545 1605 1665 1725 1785 1001 1845 1061 1905 1121 1965 1245 1365 1425 1305 941 821 881 401 461 521 581 641 701 761 geaccircarccccrcraagcrcrrraacrccaagrrcrrraraagacagcraargaaga GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA GCCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA CTTTTGAATTTGGGGGGGGGGGGGGGTCCCCTACGAGGTCGGCTTCCCCAAGTACG CTITICALITICACIONE CONTROLLA CONTROLL GGGCCTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA CAATGACTTCCCTGTATGGGCAGCTGGCTGGCTGAAGGAGCTGGGCCTCTTGGATTGCG CAGAGTGGTCTCAGAAGACCTGGCAGGCCCACTGAGTTGCTGAAGACCCAGGTGACA 1606 AGCGTGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG CGCTGCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTC CGCTGCTGCATGAGCCCCATGATCACAAGCTCTCAGATCAACAGGGCCCTGAGCTC ATGGCCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA ATGGCCAGAAACCCTCTGCCCATCTACTGTGCCCTCAACACCCAAAGGGCAGAGGCTGACCA GACTGAGGGAGCTGGCCGTGCGACTGGGCCTTCGGGCCCTGTGCAGAGGAGCAGGCCTTCC 1186 GACTGAGGGAGCTGGCCGTGCGCTTCGGGCCCTGTGCAGAGGAGCAGGCCTTCC ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGATCCGGG ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGGGATCCGGG CAATGACTTCCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCCTCTTGGATTGCG TCTCCTACATCACCGGGGCCTCGGGCTCCACCTGGGCCTTGGCCAACCTTTATGAGGACC rerectacarcacegesecressericaceressecrissectacerateaecace CAGAGTGGTCTCAGAAGGACCTGGCAGGCCCCACTGAGTTGCTGAAGACCCAGGTGACCA AGAACAAGCTGGGTGTGCTGGCCCCCAGCTGCAGCGGTACCGGCAGGAGCTGGCCG AGCGTGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG Gaps Length 3085; 33; A - 959 C; 907 G; 612 T; 0 U; 0 Other; Indels 4; 2; DB Score 1816.8; Pred. No. 0; 0; Mismatches . 4. % % ive 82. 98. Sequence 3085 BP; 607 Conserva Similarity tches 1861; 942 1786 1062 1246 1666 1726 1002 342 402 1306 1366 582 1426 642 1486 702 762 822 882 462 522 Match Query Op g Db δ qq ò g δ В 8 δ g δ qq ð Ωp δ Ωp qq õ ∂ δ

2168 2505 1601 1661 1361 1421 2265 1481 1541 1301 2926 GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGGTAAGGAGGCCAAGCCCATTTGTGTAATC ACCCAAAACCCCCCCGGCCTGTGTTTTCCCTTTCTGCGCTACCTTGAGTAGTTGGAGC AGTGCTTCAGACCTCGGGCTCAGGTGGCACTGTCCCAGGGTCCAGGCTGAGGCTGGGA GCTCCCTTGCGCCTCAGCAGTTTGCAGTGGGGTAAGGAGGCCAAGCCCATTTGTGTAATC TCTCGCCCAGCCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACCTTCTCCGACCCCA TCTCGCCCAGCCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCA CTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGGACA CTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGGACA AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC cacceeraacretearreceresersecresersesessessesses de references AGTECTTCAGAGCCTCGGGCTCGAGTGGCACTGTCCCAGGGTCCAGGCTGAGGGCTGGGGA AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAGGCTACTTTCAGCATCCTC **ACTICICCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGACACCCTCGG** recaseastrecaserecressecestrerseceasesaseases recenteceaecea cerececesasececrises is a contractiva en contractiva ----TCCTCTGGGGTCCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGGTGAACCTGT TGCGCCAGGCAGTGCAGCGGAGGCGCAGCGCAGGCCCCACTGATGGCCGGGGCCCCTGC CACCCCTAACTCTATTCCATTCCCTGGCTGCTTGCAGGTGGGGAACTGTCATCACGC AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC TGCAGCCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCT Accrecadeacadecriaracregecercadeceadeceagereregeaceeregerea GGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCT CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC

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Phospholipase A2; PLA2; antiinflammatory; inflammatory condition; rheumatoid arthritis; psoriasis; asthma; cytosolic PLA2; cPLA2; ss
3046 ACTIGATACATCACAGACTCATACAAAAAAAAAAA 3081
                                                                       Phospholipase A2 (PLA2) mRNA sequence SEQ ID NO:4
                                                                                                                                                                                         Pickard RT,
                                    AAF75000 standard; mRNA; 3085
                                                                                                                                                           97US-0041264P.
97US-00827208.
                                                                                                                                                     96US-0014608P.
                                                                                                                                         07-FEB-2000; 2000US-00500358
                                                            (first entry)
                                                                                                                                                                            (ELIL ) LILLY & CO ELI
                                                                                                                                                                                         Kramer RM,
                                                                                                                                                                                                    WPI; 2001-256372/26.
                                                                                                                US6197569-B1.
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                                                            23-MAY-2001
                                                                                                                            06-MAR-2001
                                                                                                                                                                                        Choiu XC,
                                                AAF75000;
                        RESULT 5
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useful in Novel nucleic acid molecules encoding phospholipase A2 enzyme, us screening assays for identifying compounds that inhibit or block phospholipase A2 enzyme activity.

Strifler

Sharp JD,

Disclosure; Col 57-62; 32pp; English.

The present invention describes an isolated polynucleotide (I),

Comprising a 3085 base pair phospholipase A2 (PLA2) sequence (given in

AAFA499), encoding a 913 residue phospholipase A2 protein sequence

Given in AAB74635), or a nucleotide sequence which hybridises under

Stringent conditions to the above mentioned nucleotide sequence. Also

described are: (I) an isolated polynucleotide (II) comprising an B317

Comprising (I) and an expression control sequence; (3) a host cell

comprising (I) and an expression control sequence; (IV) comprising (II)

Comprising (I) and expression control sequence; and (5) a host cell

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Sequence 3085 BP; 607 A; 959 C; 907 G; 0 T; 612 U; 0 Other;

DB 4; Length 3085;

401 GACTGAGGGAGCTGGCGACTGGGCTTCGGGCCCTGTGCAGAGGAGCAGCCTTCC Gaps 2; Indels Query Match
82.4%; Score 1816.8;
Best Local Similarity 78.9%; Pred. No. 0;
Matches 1496; Conservative 365; Mismatches 342

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                     462 ACCIGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGATCCGGG
                                                                                       CAATGACTTCCCTGTATGGGCAGCTGGCTGGAGGAGCTGGGCCTCTTGGATTGCG
                                                                                                                                  TCTCCTACATCACCGGGGCCTCGGGCTCCACCTGGGCCTTGGCCAACCTTATGAGGACC
                                                                                                                                                                              CAGAGTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA
                                                                                                                                                                                                                         702 AGAACAAGCIGGGIGIGCIGGCCCCCAGCIGCAGCGGIACCGGCAGGAGCIGGCCG
                                                                                                                                                                                                                                     762 AGGTGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG
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The present sequence is that of human mRNA encoding a novel phospholipase A2 (PLA2, also referred to bPLA2 or PLA2-beta). PLA2 liberates arachidonic acid from phospholipids, leading to the production of eloosanoids involved in inflammatory reaction. A claimed assay for evaluating the effectiveness of a compound as an inhibitor of phospholipase A2 (PLA2) involves culturing a cell transformed with an expression vector comprising PLA2 genomic DNA or CDNA, isolating the PLA2 contacting it with a candidate compound, and determining whether the PLA2 activity has been inhibited. The assay provides rapid and efficient screening for new antiniflammatory drugs that inhibit the efficient screening for new antiniflammatory drugs that inhibit the arachidonic acid cascade. These may be especially useful in the treatment of the inflammatory component of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            822 CGCTGCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTC 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       762 AGCGTGCCCGCTTGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTGCAGGAGGATGAGATCCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGATCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 GACTGAGGGAGCTGGCGTGCGACTGGGGCTTCGGGCCCTGTGCAGAGGAGCAGGCCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s to evaluate the effectiveness of inhibitors of phospholipase to screen candidate compounds, comprise recombinant expression phospholipase A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3085 BP; 607 A; 959 C; 907 G; 0 T; 612 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.4%; Score 1816.8;
ilarity 78.9%; Pred. No. 0;
Conservative 365; Mismatches
                                                                                                                                      Sharp
                                                                                                                                                                                                                                                            Disclosure; Col 58-62; 32pp; English.
                                                                                                                                       RI,
                                                                                                                                       Pickard
                                                   96US-0014608P.
97US-0041264P.
97US-00827208.
                         2000US-00498809
                                                                                                            (EFIF ) FIFFX & CO EFI
                                                                                                                                       Kramer RM,
                                                                                                                                                               WPI; 2001-366537/38.
P-PSDB; AAB82415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                            07-FEB-2000;
                                                                   19-MAR-1997;
28-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 1496;
05-JUN-2001
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2986 ACCCAAAACCCCCCGGCCCGGGCCGGUUUUCCCUUCUGCGCUACCUUGAGUAGUUGGAGC 3045 The present sequence is that of human cDNA encoding a novel phospholipase A2 (PLA2, also referred to bPLA2 or PLA2-beta). PLA2 liberates are chidonic acid from phospholipids, leading to the production of elosanoids involved in inflammatory reaction. A claimed assay for evaluating the effectiveness of a compound as an inhibitor of phospholipase A2 (PLA2) involves culturing a cell transformed with an expression vector comprising PLA2 genomic DNA or cDNA, isolating the Assays to evaluate the effectiveness of inhibitors of phospholipase A2, used to screen candidate compounds, comprise recombinant expression of novel phospholipase A2. Phospholipase A2; PLA2; bPLA2; PLA2-beta; inhibitor; screening; antiinflammatory; human; Alzheimer's disease; therapy; ss. Sharp JD, Strifler BA; 2204

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                PLA2, contacting it with a candidate compound, and determining whether the PLA2 activity has been inhibited. The assay provides rapid and efficient screening for new antiinflammatory drugs that inhibit the arachidonic acid cascade. These may be especially useful in the treatment of the inflammatory component of Alzheimer's disease
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                                                      Calcium-independent cytosolic phospholipase A2-beta; cPLA2-beta; mutant; U937 cell; membrane phospholipid turnover; intracellular signalling; arachidonic acid cascade; inflammatory disorder; rheumatoid arthritis; psoriasis; asthma; inflammatory bowel disease; antiinflammatory; ss.
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                                cDNA encoding cPLA2 N-terminal peptide-cPLA2-beta fusion protein.
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                                                                                                                                                  The invention relates to a purified phospholipase enzyme (calciumindependent cytosolic phospholipase A_2-beta enzyme) peptide appearing as ABG76482 encoded by a polymuclectide appearing as ABG764883. The protein has an enzymatic activity in a mixed micelle assay (MMA) with 1-palmitoylassaying chemical agents for antiinflammatory activity mediated by the various components of the arachidonic acid cascade. cPLA2-beta is also useful in the development of polyclonal and monoclonal antibodies which are useful as research or diagnostic tools, and to study phospholipase A_2 activity and inflammatory conditions. The present sequence encodes
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Novel purified calcium-independent cytosolic phospholipase A2-beta enzyme, useful for screening compounds having antiinflammatory activity mediated by the arachidonic acid cascade.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium-independent cytosolic phospholipase A2-beta; cPLA2-beta; U937 cell; membrane phospholipid turnover; intracellular signalling; arachidonic acid cascade; inflammatory disorder; rheumatoid arthritis; psoriasis; asthma; inflammatory bowel disease; antiinflammatory; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4183 BP; 983 A; 1177 C; 1168 G; 850 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "cPLA2-beta enzyme"
/note= "This sequence lacks a start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Partial cDNA encoding human cPLA2-beta enzyme.
2669 ACTIGATACATCACAGACTCATACAAA 2695
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 Qy

 Db
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	RESULT 11 ABX11883 ID ABX11883 standard; CDNA; 4183 BP. XX AC ABX11883; XX DT 10-MAY-2003 (first entry) XX XX DT A-CAPA-2003 (first entry) XX XX XX XX XX XX XX XX XX XX XX XX XX
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The invention relates to a purified phospholipase enzyme (calcium-independent cytosolic phospholipase A_2-beta enzyme) peptide appearing as ABG76482 encoded by a polynuclectide appearing as ABK118893. The protein has an enzymatic activity in a mixed micelle assay (MMA) with 1-palmitoyl 2-(~1~4C)-arachidonyl- phosphatidylcholine. CPLA2-beta is useful for vasaying chemical agents for antiinflammatory activity mediated by the various components of the arachidonic acid cascade. CPLA2-beta is also useful in the development of polyclonal and monoclonal antibodies which are useful as research or diagnostic tools, and to study phospholipase A_2 activity and inflammatory conditions. The present sequence encodes a
                                                                                                                                                                                                                                                                Novel purified calcium-independent cytosolic phospholipase A2-beta enzyme, useful for screening compounds having antiinflammatory activity mediated by the arachidonic acid cascade.
   "No start codon shown"
                                                                                                                                                                                                                                                                                                                           Claim 1; Col 11-14; 19pp; English.
                                                                                        2001US-00895547
                                                                                                                   97US-00788975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           partial cPLA2-beta protein
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Matches 1851, Conservative
   /note=
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                                                                                                                                                                                                                      WPI; 2003-287361/28
                                                                                                                                                                                                                                       P-PSDB; ABG76482
                                                                                                                                                                                          Kriz R, Song C;
                                                                                     29-JUN-2001;
                                                                                                                   24-JAN-1997;
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                             US6482625-B1
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2412 2472 ij 2652 2713 AGCGTGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG 2772 401 461 521 641 761 821 GACTGAGGGAGCTGGCCGTGCGACTGGGCCTTCGGGCCCTGTGCAGGAGCAGGCCTTCC ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGATCCGGG TCTCCTACATCACCGGGGCCTCGACCTGGGCCTTGGCCAACCTTTATGAGGACC ACCTGCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGGATCCGGG CAATGACTTCCCTGTATGGGCAGCTGGCTGGAGGAGGTGGGCTCTTGGATTGCG CAGAGTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA AGAACAAGCTGGGTGTGCTGGCCCCCAGCCAGCTGCAGCGGTACCGGCAGGAGCTGGCCG AGCGTGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG Gaps 33; Length 4183; Sequence 4183 BP; 983 A; 1177 C; 1168 G; 850 T; 0 U; 5 Other; 3; Indels DB 7; 82.0%; Score 1806.2; 98.1%; Pred. No. 0; ive 0; Mismatches 2533 2593 2653 762 2473 582 642 702

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2892 CTITICAATITIGGGGAGTGCGAGTICTCTCCCTACGAGGTCGGCTTCCCCAAGTACG 1001 1061 2952 3072 1241 1121 1181 1361 1421 3372 1481 3492 3612 1661 941 3793 AGCIGCIGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC 3852 1809 AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAAGGCTC 1868 CGCTGCTGCATGATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTC 2773 décrecrateareacececareareacerereaecrereaeareaececereaere 2833 ATGGCCAGAACCCTCTGCCCATCTACTGTGCCCTCAACCACCAAAGGGCAGAGCCTGACCA 2953 GGGCCTTCATCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA 2893 CTTTTGAATTTGGGGGAGTGCGAGTTCTCTCTCCTACGAGGTCGGCTTCCCCAAGTACG GGGCCTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 3013 GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 1122 ACCICCAGGACAGCITATACTGGGCCTCAGAGCCCAGCCAGCTTCTGGGACCGCTGGGTCA 1182 GGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCT CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC 3253 AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 1362 ACTICICCACAIGGAAAGCIACCACTCIGGAIGGGCICCCCAACCAGCIGACACCTCGG ACTICICCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGACACCTCGG 3133 GGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGAAGAAGAACCACCCT 3193 CAACAGCCGGCAGGATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC AGGCCACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTC 3553 TCTCGCCCAGCCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCA TGCAGCCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCT TCTCGCCCAGCCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACCCTTCTCCGACCCCA 3733 cricarcegacreciceracecracedadereaceracedecadeacedeace coreccessascenteces de la contraction de la contr ----TCCTCTGGGGTCCGGCGGACACCCGAGGGCGGCAGCTGGGGAGGTGAACCTGT 3673 ACTCGGCCCCTGGGGTCCGGCGGACACCCGAGGAGGCGGCAGCTGGGGAGGTGAACCTGT CCTGCCCCGGAGCCCCTGCGGTGCTGCACTTT-----882 942 1062 1002 1242 1302 3313 1422 3373 1482 1542 3493 1662 3613 1602 1694 g à 임 ò q à 셤 ð g 쉽 ò 셤 qq ò à à g Š q ð g ò 임 ઠે g à g 셤 임 à δ à ద ò

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       TGCGCCAGGCAGTGCAGCGGAGGCGGCAGCCCCCACTGATGGCCGGGGCCCCTGC 1928
                       CACCCCTAACTCTTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC
                                                                                   CACCCCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC
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(HUMA-) HUMAN GENOME SCI INC.

Brewer LA; Greene Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC; Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, G; Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;

WPI; 1998-609887/51

P-PSDB; AAW75132

New isolated human genes and the secreted polypeptides they encouseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.

Claim 1; Page 229-230; 447pp; English.

This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion corporated to the human protein only. The invention relates to 70 novel genes and theh human protein only. The invention relates to 70 novel genes and their fragments (nucleic acid sequences: AAV34154-V34276, amino acid sequences AAW75057-W75179) which are useful for preventing, treating acid sequences and their genes and their genes and their sequences and protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polyprotides in a sample or by determining the presence of mutations in the new polyprotides. Specific uses are described for each of the 70 polyprucleotides, based on which tissues they are most highly expressed in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct PI field.)

Sequence 1925 BP; 388 A; 613 C; 545 G; 377 T; 0 U; 2 Other;

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405 465 125 585 245 645 305 705 365 765 425 885 65 AGGGAGCTGGCCGTGGGCTTCGGGCCCTGTG-CAGAGGAGCAGCCTTCCTGAG GCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGATCCGGGCAAT GACTICCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCCTTTGGATTGCGTCTC GCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGGAGATCCGGGCAAT CTACATCACCGGGGCTCCACCTGGGCCTTGGCCAACCTTTATGAGGACCCAGA GTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAA CAAGCTGGGTGTGTGCCCCCCAGCCAGCTGCAGCGGTACCGGCAGGAGCTGGCCGAGCG GCTGCATGATGAGCCCCATGATCACAGGTCTCAGATCAACGGGAGGCCCTGAGTCATGG TGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGGGGT Gaps 34; 81.2%; Score 1788.8; DB 2; Length 1925; llarity 97.9%; Pred. No. 0; Conservative 1; Mismatches 4; Indels 34; 4; Indels Query Match Best Local Similarity Matches 1844; Conserv 246 9 90 99 466 126 526 586 306 366 646 904 826

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1065 1125 TGAATTTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGCTTCCCCAAGTACGGGGC 1005 1185 1245 1365 1305 1025 1485 1145 1605 1665 605 1445 1812 725 845 1505 1872 1565 905 GCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTCATGG CCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAAGGGCAGAGCCTGACCACTTT 546 CCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAGGCAGAGCCTGACCTCTTT CCAGGACAGCTTATACTGGGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGGTCAGGAA 906 AGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCCAGGC CTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGGCT TCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCAACCT CCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTTCTGAAGATAGAAGCACCACCTCAAC 846 CCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCCTCAAC AGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCCAGGC CACACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTCACTT CTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGACACCCTCGGAGCC CCACCTGTGCCTGCATGTTGGCTACCTCATCATACCAGCTGCCCTCCTCTGCA CACACATAATTICCTGCGTGGCCTCCATTTCCACAAAGACTACTTTCAGCATCCTCACTT GCCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCTTCCA GCCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCACGGAGCCTTCCA CTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCCCAAACCAGCTGACACCTCGGAGCC ccccedadecccriscerecreterrine recordedacte contracted co 1386 GGCCCCTGGGGTCCGGCGGACACCCGAGGAGGCGCAGCTGGGGAGGTGAACCTGTCTTC 1566 CCAGGCAGTGCAGCGGAGAGGCGCAGCGCACCATGATGGCCGGGGCCCCTGCCACC GCCCAGCCCCGAAGAGCAGCTCCAGCCTCGGGAGTGCCACACCTTCTCCGACCCCAC 1694 -TCCTCTGGGGGTCCGGCGGACACCCGAGGCGGCAGCTGGGGGAGGTGAACCTGTCTTC 1813 GCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTCTGCG 1506 GCTGCACCTGACACATACAATGCTGCAACAACCAGGAGCAGCTGCTGGAGGCTCTGCG CCAGGCAGTGCAGCGGAGGGGCAGCGCAGCCCCACTGATGGCCGGGGCCCCTGCCACC ATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGGACAAGCT 946 1006 999 1066 1126 909 1186 1246 1306 1366 1026 1426 1086 1486 1146 1546 1206 1666 1326 1446 996 1753 1873 ò qq ò 셤 δ ద à g q ద Dp à ò à ò 셤 ₽ g ò g ò g ₽ 원 δ g ð a g ò à d à g 8

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                                                                  CTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCCAGGCTGAGGGCTGGGGAGCTC
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97US-0040334P.
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97US-00403311P.
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         RUBEN S M.
ROSEN C A.
FISCHER C L.
                   SOPPET D R.
CARTER K C.
BEDNARIK D R
                                                             OLSEN H S.
EBNER R.
BREWER L A.
                             ENDRESS G A
                                             GREENE J M.
FERRIE A M.
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                                                          FLORENCE K
                                          YOUNG P E.
                                       FENG P.
                                                    DUAN R.
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                                (YUGG/)
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Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC; Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM; Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;

P-PSDB; ABO02008.

Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing or treating deficiencies or disorders of the immune system, autoimmune disorders, hyperproliferative disorders, and infectious diseases.

Claim 4; Page 130-131; 243pp; English.

The invention describes an isolated human secreted HODAZSO polypeptide from comprising a sequence at least 95% identical to a sequence selected from polypeptide fragment of any one of the 122 polypeptide sequences of PS, fully defined in the specification and having biological activity, polypeptide domain or spelicipe of PS, full-length according to protein of PS, or variant, allelic variant or species homologue of PS. (I) or a polymucleotide (II) amonding (I) is useful for preventing, treating, or ameliorating a medical condition in a mammalian subject. (I) is also useful for diagnosing a pathological condition or a subject. (I) is useful for independent of the polypeptide with the binding partner and determining whether the binding partner which involves contacting the polypeptide with the binding partner which involves contacting the polypeptide with the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding of partner and deficiency disorders of hamatopoletic cells, to treat immunologic deficiency disorders of hamatopoletic cells, to treat immunologic deficiency disorders, thrombocytopenia or hemoglobinuria, blood for disorders, blood platelet disorders, autoimmune disorders and wiskott-Aldrich disorders, blood platelet disorders, autoimmune disorders dermatitis, glomenlombritis, Grave's disease), allergic reactions, and dermaticis, glomenlombritis, Grave's disease), allergic reactions, cells and disorders, benchylic anamina, rhemmacoid architistic, partner diseases (e.g., viral, partnerial, fungal or parasitic infection), central and peripheral nervous system diseases (e.g., spinal coorders in the abdomen, bone, breast, disease), allergic reactions, system diseases (e.g., spinal code disorders, head trauma or stroke), to differentiate, proliferate and attract cells leading to herself mammalian catabolism affecting additive or preservative, processing, utilisation, as a food addit

ប្ដុ	c sequence encodes a novel human secreted protein	
S S	Sequence 1925 BP; 388 A; 613 C; 545 G; 37	
Qu Be Ma	Query Match 81.2%; Score 1788.8; DB 7; Length 1 Best Local Similarity 97.9%; Pred. No. 0; Matches 1844; Conservative 1; Mismatches 4; Indels	25; 4; Gaps 2;
δ	347 AGGAGCTGGCCGTGCGACTGGGCTTCGGGCCCTGTG-	TTCCTGAG 40
q	6 AGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCCTGTG	rccrgag
ò	by 406 CACGAGGAAGCAGGTGGCCGCGGGCCTTGAGGCAGCCCTGCAGCTGGATGGA	4
Ор	66 CAGGAGGAAG	GGAGACCT 125
δλ	4	CGGGCAAT 525
q	126 GCAGGAGGA	CCGGCCAAT 185
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qq	186 GACTICCCT	: TGCKTCTC 245
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AAV34164 standard;

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis, tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; niflammation; ischaemic shock; Alzheimer's disease; restenosis; AlDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoprosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC; Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM; Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA; Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;

WPI; 1998-609887/51 P-PSDB; AAW75067 New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.

Claim 1; Page 171-172; 447pp; English.

This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC oportion (e.g. AAV34145) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 70 novel genes and their fragments (mucleic acid sequences: AAV34184-V34276; amino acid sequences AAV35057-W75179) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, by the propertides in a sample or by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypuclectides. Specific uses are described for each of the continuation of the search of the continuation of the content of the continuation of the continuation of the continuation of the content of the co field.) (Updated on 25-MAR-2003 to correct PI field.)

Sequence 1926 BP; 388 A; 613 C; 545 G; 377 T; 0 U; 3 Other;

3; 1005 1065 1305 465 525 1125 1185 CACACATAATTTCCTGCGTGGCCTCCATTTCCAAAAAACTACTTTCAGCATCCTCACTT 1365 125 585 245 645 305 705 365 765 425 825 485 885 945 CCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCTCAAC 1025 605 665 65 785 845 905 965 347 AGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCCTGTG-CAGAGGAGCAGCCTTCCTGAG 6 Addadcirdecerrecearrecearrecearcererrecearecarecenecerrecreas 66 checadecadecadecrecececereritadecadecerecadecrecadardeadacer CTACATCACCGGGGCCTCGGGCTCCACCTGGGCCTTGGCCAACCTTTATGAGGACCCAGA GTGGTCTCAGAAGGACCTGGCAGGCCCCACTGAGTTGCTGAAGACCCCAGGTGACCAAGAA CAAGCTGGGTGTGCTGGCCCCCCAGCCAGCTGCGGTACCGGCAGGAGCTGGCCGAAGCG GCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTCATGG CCAGAACCCTCTGCCCATCTACTGTGCCCTCAACCACCAAAGGGCAGAGGCCTGACCACTTT GCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGGGATCCGGGCAAT GACTICCCIGIAIGGGCAGCIGGCIGGCCIGAAGGAGCIGGGCCICIIGGAIIGCGICIC TGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGGCGCT GCTGCATGATGAGCCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTCATGG CCAGGACAGCTTATACTGGGCCTCAGACCCAGCCAGTTCTGGGACCGCTGGGAA TGAATTTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCGGCTTCCCCCAAGTACGGGGC 606 TGAATTTGGGGAGTGCGAGTTCTCTCCCTACGAGGTCGGCTTCCCCAAGTACGGGGC CTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGGCT 1066 TCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCAACCT AGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCCAGGC Gaps 726 rechéadrecedenterderretradaaderareregadecadecrerarededeceader 906 AGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCCAGGC 966 CACACATAATITCCTGCGTGGCCTCCATITCCACAAAGACTACTTTCAGCATCACTT 35; Length 1926 4; Indels DB 2; Score 1777.8; Pred. No. 0; 1; Mismatches 80.78; Matches 1844; Conservative Query Match Best Local Similarity 466 526 989 646 306 999 907 366 994 426 826 988 946 1006 1126 846 1186 1246 1306 ਨੇ d à g ò a à 엄 셤 g à 8 à Ωp δ g ò 셤 ò 셤 à d à g à 엄 ò d 8 임 à q 8

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Rosen CA, Fischer CL, Soppet DR, Carter KC;
R, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA; DR, bu Bednarik DR Ferrie AM, Ruben SM, Shi Y;

2003-466138/44. P-PSDB; ABO01943. Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing or treating deficiencies or disorders of the immune system, autoimmune

Line introduction describes an isolated human secreted HODAZSO polypeptide from polypeptide fragment of any one of the 123 polypeptide sequences of from polypeptide fragment of any one of the 123 polypeptide sequences of 124 polypeptide domain or epitope of Ps, secreted form of Ps, fully defined in the specification and having biological activity protein of Ps, or variant, allelic variant or species homologue of Ps. (T) or a polymucleotide (II) encoding (I) is useful for preventing, or ameliorating a medical condition in a mammalian subject. (I) is useful for identifying a binding partner which involves contacting the polypeptide with the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding partner and determining whether the binding corders, ataxia telangiectasia, HIV infection, coagulation disorders, blood plateled disorders, autoimmune disorders (e.g., Addison's disease, haemolytic anaemia, rheumatoid architis, grave's disease, blood plateled disorders, intentions of coatted in the abdomen, bone, breast, diseases (e.g., viral, coatterial, fungal or parasitic infections diseases (e.g., viral, torgal or parasitic infections diseases (e.g., viral, torgal or parasitic infections diseases (e.g., viral, coatterial, fungal or parasitic infections, central and parameterial, replace or protect tissue damaged by parameterial, replace or protect tissue damaged by the disea metabolism affecting catabolism, anabolism, processing, utilisation, and storage of energy, to change a mammel's mental state or physical state, or as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. This sequence encodes a novel human secreted protein The invention describes an isolated human secreted HODAZ50 polypeptide disorders, hyperproliferative disorders, and infectious diseases. Claim 4; Page 85-86; 243pp; English. $\mathbb{Z} \times \mathbb{Z} \times$

Sequence 1926 BP; 388 A; 613 C; 545 G; 377 T; 0 U; 3 Other;

405 465 chacarcacedesectrossecrecacereses as 305 705 65 GTGGTCTCAGAAGGACCTGGCAGGCCCACTGAGTTGCTGAAGAGCCCAGGTGACCAAGAA 365 CAAGGTGGGTGTGGTGGCCCCAGCTGCAGCGGTACCGGCAGGAGCTGGCGAAGC 347 AGGGAGGTGGCCGTGCGACTGGGGCTTCGGGCCCTGTG-CAGAGGAGGAGGCCTTCCTGAG 6 AddaActidGcCGTGCGACTGGGCTTCGGGCCCTGTGCCAGAGGAGCANGCCTTCCTGAG GCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGATCCGGGCAAT 186 GACTTCCCTGTATGGGCAGCTGGCTGGCTGAAGAAGAGCTGGGCCTCTTGGATTGCKTCTC CTACATCACCGGGGCTCGACCTCGGGCCTTTGGCCAACCTTTATGAGGACCCAGA GTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAA GCAGGAGGATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGATCCGGGCAAT GACTICCCIGIAIGGGCAGCIGGCTGGCCTGAAGGAGCTGGGGCCTCTTGGATTGCGTCTC Gaps 80.7%; Score 1777.8; DB 7; Length 1926; 97.9%; Pred. No. 0; 4; Indels 35; Query Match 80.7 Best Local Similarity 97.9 Matches 1844; Conservative 466 526 126 586 246 646 306 904 ò ò 셤 ð 음 ä 셤 ð g ò 유

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	18	87			BC013415	BC013415	Homo sap
	1806	82			AR168355	AR168355	Sequence
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  Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Patent: US 6242206-A 2 05-JUN-2001;
Location/Qualifiers 1. .3085 /organism="unknown" /wol_type="unassigned DNA" Query Match
Best Local Similarity 98.2%;
Matches 1861; Conservative GACTGAGGGAGCTGG 342 462 1486 582 642 702 1606 822 1666 882 1726 1002 1966 762 942 1786 1062 1906 1122 2026 1182 source TITLE JOURNAL FEATURES ORIGIN 셤 ò ð 셤 ò a à ద ò g ò qq ò qq ઠે g ò Db ò qq õ g δ СP à QQ ò qq g ò

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DEFINITION
ACCESSION

GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 1121 1906 GGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCA 1965 1485 1605 1665 1001 CCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA 1061 GATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTC 1725 CCTCTGCCCATCTACTGTCCCTCAACACCAAAGGCAGAGCCTGACCA 1785 ; CCTCTGCCCATCTACTGTGCCCTCAACACCAAGGGCAGAGCCTGACCA 941 641 701 761 821 881 581 521 ACCGGGGCCTCGGGCTCCACCTGGGCCTTGGCCAACCTTTATGAGGACC GGTGTGCTGGCCCCCAGCCAGCTGCAGCGGTACCGGCAGAGCTGGCCG TTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGGCCCTCATCAACGAGG GGGGAGTGGTGCGAGTTCTCTCTCCCTACGAGGTCGGCTTCCCCCAAGTACG BATGAGATCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGGGATCCGGG CAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCAGGTGACCA TTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAACGAGG GATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTC CTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCCTCTTGGATTGCG ACCGGGGCTCCACCTGGGCCTTGGCCAACCTTTATGAGGACC CTRECCETECGACTEGGCTTCGGGCCCTGTGCAGAGGAGCAGGCTTCC Gaps lipase A2 and related nucleic acid compounds 42206-A 4 05-JUN-2001; tion/Qualifiers o 3085) , Kramer,R.M., Pickard,R.T., Sharp,J.D. and 33; DB 6; Length 3085; 2; Indels 82.4%; Score 1816.8; 98.2%; Pred. No. 0; tive 0; Mismatches type="unassigned DNA" anism="unknown" :15125075 1062 Ωp ò δ

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Db 3046 ACTTGATACATCACAGACTCATACAAAAAAAAA 3081 RESULT 6	AF065215 LOCUS JOCUS JOCUS DEFINITION Homo sapiens cytosolic phospholipase A2 beta (cPLA2 beta) mRNA, complete cds. ACCESSION AF065215 VERSION AF065215. GI:3811346	Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebr Mammalia; Eutheria; Primates; Catarrhini; Homir E 1 (bases I to 3352) S Pickard, R.T., Strifler, B.A., Kramer, R.M. and SP	ILLE MOLECULAT CLOUING OF TWO New Numan paralogs of 85-kDa cytosolic phospholipase A2 JOURNAL J. Biol. Chem. 274 (13), 8823-8831 (1999) MEDLINE 99185108 PUBMED 10085124 REFERENCE 7 (hares 1 to 3352)	Pickard, R.T., Control of the contro	= ·· + E m	/gene="CPLA2 beta" 163054 /gene="CPLA2 beta" /codon start=1 /product="Cytosolic phospholipase A2 beta"	/protein_id="AAC78836.1" /db_xref="Gi1:3811347" /translation="MABAALEAVKSELREFPAAARELCVPLAVPYLDKPPTPLHFYRD WVCPNRPCTIRNALQHPVALOKWSLPYFRATVGSTEVSVAVTPDGYADAVRGDRFMP AERRLPLSFVLDVLEGRAQHPGULYVQKQCSNLPSELPQLLPDLESHPWASERLGKM PDAVNFWLGBAAAVTSLHKDHYENLYCVVSGEKHFLFHPPSDRPFIPYELYTPATYQL TEGGTFRVVDREGRARVSTCLLTVRYLQARLFSKDLVPTPSDCYTTLMLPFACSH BIOTOPRETRYSGEGRARMSEVGERDSTEDGERDGYTTPATYQL	AGETRRESES Y WAUGSTER HARQLANGELANGELDUYTEDDYJLSYLFEDAGTER AGETRRESESSES Y WAUGSTER HARQLANGELDNGEWILVSRIGHTED FULSYLFEDAGTER AGESTRRESESSES SE Y WAUGSTER HARQLANGEWILVSRIGHTED FULSYLEDGESTEG QKSSEHRVQL VVPGSCEGPQEASVGTGFRFRHCPACWEGESTRLQDAFEGOLKAPLS ALPSGOVYRLVPPTSQEPLARVELKEAGIRELAVRLGFGPCAEEQAFLSRRKQVVAA ALRQALQLGGDEI PYVA INATGGGI RAMTSLYGGAGIREIGLLCVSYI TGAS GSTWALLANLYEDPEWSQKDLAGPTELLKTQVTKNKLGYLAPSQLORYRGGSLTAFEF YBSCFTNIWALLINBALLHDEPHDHKLSDQREALSHGONPLPTYCALNFRGGSLTTFFF GEWCEFSPYEVGFPKYGAFI PSELFGSEFFMGQLAMKRLPESRI CFLEGIWSNI YAANL	QUSLYMASEPSQUENTRYNQANLDKEQVPLLKTEREPSTAGRIAEFFTDLJFWRPLA QATHNFLRGLHFHKOYFQHFHFSTWKATTLDGLPNQLTPSEPHLGLLDVGTJRTSCL PLLQPTRYDDLJLSLDYNTHGAFSTWGTTLDGLPNQLTPSEPHLGLLDVGTJRTSCL FLDPTRYDDLJLSLDYNTHGAFOQLGLGRFCOEQGIPFPISPSEBGLQPRECHT FSDPTCPGAPAVLHFPLVSDSFREYSAPGVRRTPEEAAAGEVNLSSSDSPYHTKVTY SQEDVDKLLHLTHYNVCNNQEQLLEALRQAVQRRRQRRPH"	Ouery Match Query Match Best Local Similarity 98.0%; Pred. No. 0; Matches 1859; Conservative 2; Mismatches 2; Indels 33; Gaps 1; Oy 342 GACTGAGGAGCTGGCCGTGCGCTTCGGCCCTGTGCAGAGAGCAGGCCTTC 401
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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Halle, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Bachez, A., Whitlang, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G. G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schuutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.govSeries: IRAL Plate: 11 Row: a Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: He I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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On Aug 12, 2003 this sequence version replaced gi:16807142.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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Kriz,R. and Song,C.

Cytosolic phospholipase A2-Beta enzymes
Patent: US 6287838-A 3 11-SEP-2001;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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sapiens"

organism="Homo"

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Kriz,R.W.
Direct Submission
Submitted (21-JAN-1999) Genetics Institute, 87 Cambridge Park
Drive, Cambridge, MA 02140, USA
Drive, Candridge, MA 02140, USA
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AF121908 3339 bp mRNA linear PRI 12-OCT-1999 Homo sapiens cytosolic phospholipase A2 beta mRNA, complete cds. AF121908 AF121908.1 GI:4886977 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (base 1 to 3339)
Song. C., Chang.X.J., Bean, K.M., Proia, M.S., Knopf, J.L. and Kriz, R.W.

Kriz, R.W.
Molecular characterization of cytosolic phospholipase A2-beta
J Biol. Chem. 274 (24), 17063-17067 (1999) 2 (bases 1 to 3339) Song, C., Chang, X.J., Bean, K.M., Proia, M.S., Knopf, J.L. and Homo sapiens (human) Homo sapiens 10358058 RESULT 10
AF121908
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE PUBMED REFERENCE AUTHORS ORGANISM AUTHORS REFERENCE JOURNAL MEDLINE TITLE

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WYCPRRPCI IRNALOHWPALOKWSLPYFRATVGSTESVSVAYTPDGYADAWGDRFWMP
AERRIPESKTUDYLGGRAQHPGVLYVQKGCSMLFSELPOLLPDLESKHVPWASERAGKM
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                                                                                                                     product="cytosolic phospholipase A2 beta"
protein id="AAD32135.1"
db_xref="G1:4886978"
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98.1%; Pred. No. 0;
cive 0; Mismatches
/mol_type="mRNA"
/db_xref="taxon:9606"
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1923 GGCTGCTGCATGATCACAAGCTCTCAGATCAACGGAGGCCCTGACTC 1982 882 ATGGCCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACGGCAGAGCCTGACCA 941 1983 ATGGCCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACGGCAGAGCCTGACCA 2042 942 CTTTTGAATTTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTCCCCAAGTACG 1001 2043 CTTTTGAATTTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTTCCCCAAGTACG 1001 2044 CTTTTGAATTTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTTCCCCAAGTACG 1001 2045 CTTTTGAATTTGGGGAGTGGTGCGAGTTCTCTCCCTACGAGGTTCCCCAAGTACG 1101 2046 CTTTTGAATTTGGGGAGTGGTGCGAGTTCTCTCTTTATGGGGCAGCTGATGAAGA 1061 2103 GGCCTTCATCCCCTTTTGGAGTTCTTTTTATGGGGCAGCTGATGAAGA 1121 2104 GGCTTCCTGAGTCCCGCATTTTGGAAGGTATCTTGTAGAGCAGCTGATGAAGA 2162 1062 GGCTTCCTGAGTCCCGCATTTTAGAAGGTATCTGGAACCTGTATGCAGCCA 2222 1122 ACCTCCTGAGTCCCGCATCTTTAGAAGGTATCTGGAACCTGTATGCAGCCA 2222 1122 ACCTCCTGAGTCCCGCATCTTTAGAAGGTATCTGGAACCTGTATGCAGCCA 1121 2163 GGCTTCCTGAGTCCCGCATCTTTAGAAGGTATCTGGAACCTGTATGCAGCCA 1121 2163 GGCTTCCTGAGTCCCGCATCTTTAGAAGGTATCTGGAACCTGTATGCAGCCA 1121 2164 ACCTCCTGAGTCCCGCATCTTTAGAAGGTATCTGGAACCTGTATGCAGCCA 1121 2165 ACCTCCTGAGTCCCGCATCTTTAGAAGGTATCTGGAACCTGTATGCAGCCA 1121 2167 ACCTCCTGAGTCCCGCATCTTAGAAGGTATCTGGAACCTGTATGCAGCCA 2222 1122 ACCTCCTGAGTCCCGCATCTTAGAAGGTATCTGGAACCTGTATGCAGCCA 1121 2167 ACCTCCTAGAGTCCCGCATCTTTAGAAGGTATCTGGAACCTGTATGCAGCCA 1121 2167 ACCTCCTAGAGTCCCGCATCTTTAGAAGGTATCTGGAACCTGTATGCAGCCA 1121 2168 ACCTCCTAGAGTCCCGCATCTTAGAAGGTATCTGGAACCTGTATGCAGCCA 1121	ACTECTACATABATTICETGGGCCTCAGAGCCTTCTGGAGCTGGGGGCCTCGGGGGCCAGGGGGGGG	1482 TGCAGCCACTCGGAACGTGGACCTCTCTCTCTTCATTCAT

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1666 GCCCAGCCCCGAAAGAGCAGCTCCAGCACCCCCCACACCCTTCCCGACCCCCCCC	RESULT 14 BD195624 LOCUS DEFINITION TO human secreted proteins. ACCESSION UP195624. GI:33005394 VERSION Up195624. GI:33005394 VERSION Up195624. GI:33005394 VERSION Up195624. GI:33005394 Unidentified U
126 GCAGGAGGATGACATCCCAGTGGTAGTATTATCGCCACTGGTGGTGGATCCGGGCAAT 185 186 GACTTCCCTGTATGGCTGGTGGTGGCTGAAGGAGCTGGGCTCTTGGATTGCTCCT 245 186 GACTTCCCTGTATGGCCTCCACCTGAAGGACTGGCCTGAAGGACTGGCTTGGCTGAATTGCTCCAA 45 187 1	

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PC G1N3/50, Linear,
CC Topology: Linear,
CC 70 human secreted proteins
FH Key
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PI PING FENG, PAUL E YOUNG, JOHN M GREENE, ANN M FERRIE, ROXANNE DUAN,
PI JING SHAN HU, KIMBRELY A FLORENCE, HENRIK S OLSEN, REINHARD EBNER,
PI LAUBIE A BREWER, PAUL A MOORE, YANGGU SHI, DAN YI LI, ZHIZHEN ZENG,
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Best Local Similarity 97.9%; Pred. No. 0;
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Patent No. 6025178
GENERAL INFORMATION:
APPLICANT: Chiou, Xue-Chiou C.
APPLICANT: Kramer, Ruth M.
APPLICANT: Pickard, Richard T.
APPLICANT: Sharp, John D.
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                                                                     1606 AGCGUGCCCGCUUGGGCUACCCAAGCUGCUUCACCAACCUGUGGGCCCCUCAUCAACGAGG
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APPLICANT: Strifler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,208
FILING DATE: 28-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.4%; Score 1816.8; 78.9%; Pred. No. 0; pive 365; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION 1432
PRIOR APPLICATION NUMBER: US 60/014,608
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J
RESISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
                                                                                                                   ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center STREET: Indianapolis STATE: Indianapolis COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3085 base pairs
TYPE: nucleic acid
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linear
                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 28
CLASSIFICATION:
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Matches 1496;
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                                                                                                                                                                                                                Pred. No. 0;
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98.2%;
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 3085 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                               Query Match
Best Local Similarity 98.2
Matches 1861; Conservative
                                                                                                                                   CDS
48..2786
                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-09-500-358-2
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                       CACCCCTAACTCTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC
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        AGCTGCTGCACCTGACACTTACAATGTCTGCAACAACAGGAGCAGCTGCTGGAGGCTC
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APPLICANT: Kramer, Ruth M.
APPLICANT: Framer, Ruth M.
APPLICANT: Pickard, Richard T.
APPLICANT: Shard, John D.
APPLICANT: Strifler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: WOLLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STREET: Indianapolis
STREET: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/827,208
FILING DATE: 28-MAR-1997
APPLICATION NUMBER: US 60/014,608
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,808
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEPAX: (317) 276-3861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09500358 Patent No. 6197569 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
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                                                           CAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGGCCC
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COMPUTER: PACADA

MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
COMPUTER: THM PC compatible
COMPUTER: PACADA

SOFTWARE: PACATION DATA:
APPLICATION NUMBER: US/09/500,358

FILING DATE: 28-MAR-1997

APPLICATION NUMBER: US 60/014,608

FILING DATE: 29-MAR-1997

APPLICATION NUMBER: US 60/014,608

FILING DATE: 29-MAR-1996

PRIOR APPLICATION NUMBER: US 60/014,608

FILING DATE: 19-MAR-1997

ATTORNEY/AGBTION NUMBER: US 60/011,264

FILING DATE: 19-MAR-1997

ATTORNEY/AGBTI INFORMATION: GENERAL INFORMATION:
APPLICANT: Chiou, Xue-Chiou C.
APPLICANT: Chiou, Xue-Chiou C.
APPLICANT: Framer, Ruth M.
APPLICANT: Frickard, Richard T.
APPLICANT: Strifler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 82.4%; Score 1816.8; 78.9%; Pred. No. 0; Best Local Similarity 78.9%; Pred. No. 0; Matches 1496; Conservative 365; Mismatches United States of America ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis Sequence 4, Application US/09500358 Patent No. 6197569 REGISTRATION NOTES.

REFERENCE/DOCKET NUMBER: X-1(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEPHONE: (317) 276-0756
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs NAME: Gaylo, Paul J. REGISTRATION NUMBER: 36,808 TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: mRNA STATE: Indiana COUNTRY: United 46285 원 8

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RESULT

25.66 CUUGCCCCGGAGGCCCCUUGCGCAGCCCCCGAGCCGCACCCCCCCC	RESULT 5 US-09-498-809-2 IS-09-498-809-2 IS-09-498-809-2 IS-09-498-809-3 IS-09-498-809-3 IS-09-498-809-3 IS-08-80-80-80-80-80-80-80-80-80-80-80-80-

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                                                GGAACCAAGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGATAGAAGAACCACCT
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98.2%; Pred. No. 0;
live 0; Mismatches
                                                          X-10610
ATTORNEY FAGENT INFORMATION:
NAME: GAYLO, PAUL J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: x-106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs
STRANDEDNESS: single
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Matches 1861, Conservative
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APPLICANT: Kramer, Ruth M.
APPLICANT: Fickard, Richard T.
APPLICANT: Pickard, Richard T.
APPLICANT: Strifler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,809
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APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-WRR-1997
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/827,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana COUNTRY: United States of American States of American States of States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of American States of America
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REPERENCE DOCKET NUMBER: X-10
TELECOMMUNICATION INFORMATION:
TELEPAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs
                                                                                                                                                                                                        Sequence 4, Application US/09498809
Patent No. 6242206
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gaylo, Paul J. REGISTRATION NUMBER: 36,808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simil
Matches 1496;
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US-09-498-809-4
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1469 GGGCCTTCATCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGA 1528
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                                                                                                                                                                                                                                        Score 1806.2;
Pred. No. 0;
0; Mismatches
                 NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: 015289
TELECOMMUNICATION INFORMATION:
TELEPRAN: (617) 498-824
INFORMATION: (617) 876-581
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 2699 base pairs
                                                                                                                                                                                                                                        82.0%;
98.1%;
          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                    Best Local Similarity 98.1
Matches 1851; Conservative
                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                CTTCATCGGACTCTCCCTACCACTACACGAAGGTGACCTACAGCCAGGAGGACGTGGACA 1808
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GENERAL INFORMATION:

APPLICANT: SCAN

APPLICANT: SCAN

TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET: 87 CambridgePark Drive

CITY: CambridgePark Drive

STATE: MA

COUNTRY: USA

CONFUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Patentin Release #1.0, Version #1.30

COMPUTER: DATE:

MEDICATION DATA:

CLASSIFICATION:

PRIOR APPLICATION NUMBER: US/09/460,145

FILING DATE:

APPLICATION NUMBER: 08/788,975

FILING DATE:

APPLICATION NUMBER: 08/788,975
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Patent No. 6287838
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US-09-460-145-3
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                                                                                                                                                                                             APPLICANT: Kriz, Ron
Song, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
TUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2699;
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
CORREST: 87 CambridgePark Drive
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: man
COUNTRY: USA
COUNTRY: USA
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFRATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1806.2;
Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/895,547
FILING DATE: 29-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
2669 ACTIGATACATCACAGACTCATACAAA 2695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI5289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/460,145
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 2699 base pairs
                                                                                                                           ; Sequence 3, Application US/09895547
; Patent No. 6482625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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98.1%;
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Matches 1851; Conserv
                                                                                                                                                                                       GENERAL INFORMATION:
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                         CGCTGCTGCATGATGAGCCCCCATGATCACGAGGCTCTCAGATCAACGGGGGCCCTGAGTC
                                           2773 CGCTGCTGCATGATGAGCCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTC
                                                                                                    2833 AIGGCCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCA
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OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4183;
                                                                                                                                               MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/9895,547
FILING DATE: 29-Jun-2001
CLASSIFICATION: UNKnown>
PROM APPLICATION DATA:
APPLICATION NUMBER: 09/460,145
FILING DATE: <UNKnown>
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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                           CORRESPONDENCE ADDRESS:
RADDRESSES:
RADBRESSES:
RADBRESSES:
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
STATE: MA
ZIP: USA
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                      NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI5289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4183 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                     COMPUTER READABLE FORM:
TITLE OF NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-895-547-1
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Past Local S
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,889
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,893
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,630
ER FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,637
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,888
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,872
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,313
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FILING DATE: 1997-04-11
                                                                                                                                                                                                   APPLICATION NUMBER: 60/047,613
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,582
APPLICATION DATE: 1997-05-23
APPLICATION NUMBER: 60/047,596
                                                                                                                                                                                                                                                                                         FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,612
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,632
FILING DATE: 1997-05-23
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,314
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APPLICATION NUMBER: 60/043,569
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APPLICATION NUMBER: 60/043,672
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                                                            APPLICATION NUMBER: 60/047,500 FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,311
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APPLICATION NUMBER: 60/043,671
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APPLICATION NUMBER: 60/047,492
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,598
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                       TGCGCCAGGCAGTGCAGCGGAGGCGGCAGCGCAGGCCCCACTGATGGCCGGGGCCCCTGC 1928
                                                                     CACCCCTAACTCTCATTCCTTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC
                                                                                                                                        AGIGCITCAGAGCCICGGGCTCAGGIGGCACTGTCCCAGGGICCAGGCTGAGGGCTGGGA
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZOO1P1
CURRENT APPLICATION NUMBER: US/09/148,545
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APPLICATION NUMBER: PCT/US98/04482
FILING DATE: 1998-03-06
APPLICATION NUMBER: 60/040,162
FILING DATE: 1997-03-07
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R FILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,533
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APPLICATION NUMBER: 60/047,592
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,503
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,615
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APPLICATION NUMBER: 60/047,600
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APPLICATION NUMBER: 60/040,333
FILING DATE: 1997-03-07
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; Sequence 86, Application US/09148545
; Patent No. 6590075
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81.2%; Score 1788.8;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1844; Conservative 1; Mismatches ; BARLIER APPLICATION NUMBER: 60/057,650 ; BARLIER PILING DATE: 1997-09-05 ; EARLIER APPLICATION NUMBER: 60/056,884 ; EARLIER FILING DATE: 1997-08-22 ; NUMBER OF SEQ ID NOS: 280 ; SOFTWARE: PALENTIN Ver. 2.0 ; SEQ ID NO 86 ; LENGTH: 1925 406 466 286 646 994 1006 999 1066 426 826 486 886 546 946 909 Š ð d à d ò QQ ò g ठे qq ò a qq 8 원 상 g δ qq à g ò g ò g ò g 8

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ari	CACACALANTING COCCO	; BARLIER FILING DATE: 1998-03-06 ; EARLIER APPLICATION NUMBER: 60/040,162
λõ	CTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGGAGGCTGGGGGGGG	FILING DATE: APPLICATION N
DP	CICIGGAI GGGCI CCCCAACCAGCI GACACCC TCGGGGCCC	
ΟŊ	1426 CCACCIGIGCIGCIGGAIGTIGGCIACCICAICAATACCAGCIGCCCIGCC	
Db	1086 CCACCTGTGCTGCTGCATGTTGGCTACCTCATCAATACCAGCTGCCTGC	
ζ	1486 GCCCACTCGGGACCTCGACCTCATCCTGTCTTGGACCTACCACCCCCCACGGAGCCTTCCA 1545	
qq	1146 GCCCACTCGGGACGTGGACCTCATCCTCTCTACAACCTCCACGGAGCCTTCCA 1205	; EARLIER APPLICATION NUMBER: 60/040,334 RARLIER FILING DATE: 1997-03-07
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a a	6 GCIGCACCAGACACATIACAATGICTGCAGCAACCAACCAACCAACCAACCAACCAACCAACAACA	; EARLIER FILING DATE: 1997-05-23 ; RAPLIER APPLICATION NUMBER: 60/047,581
λŏ	3 CCAGGCAGTGCAGCGGAGG	EARLIER FILING DATE: 1997-05-23 PARLIER PILING TOTAL PARLIER FILING TOTAL PARLIER PROPILICATION NIMBER: 60/047,584
qq	GGGCAGCCCCCACTGATGGCCGGGGCCCCCTGCCACC	EARLIER FILING DATE: 1997-05-23
٥٧	1933 CCTAACTCTCATTCATTCCTGGCTGCTGAGTTGCAGGTGGGGAACTGTCATCACGCAGTG 1992	; EARLIER APPLICATION NUMBER: 00/04/,500 ; EARLIER FILING DATE: 1997-05-23
qq	1626 CCTAACTCTCATTCATTCCCTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGCAGTG 1685	; EARLIER APPLICATION NUMBER: 90/04/,50/
Š	1993 CTTCAGAGCCTCGGGGCTCAGGCACTGTCCCAGGGTCCAGGGCTGAGGCTGGGAGCTC 2052	; EARLIER APPLICATION NUMBER: 60/047,492 ; EARLIER FILING DATE: 1997-05-23
qq	1686 CTTCAGAGCCTCGGGCTCAGGTGGCACTGTCCCAGGGTCCAGGCTGAGGGCTGGGAGCTC 1745	
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Å í	A MANACCOCCCGGGCCC G G GCCCCGGCCCCGGCCCGCGCGCG	
gg	5 AAAACCCCCCGGCCTGTGCCTGTTTCCCTTCTGCGCTACCTTGTTTCTCCTCCCTC	; EARLIER FILING DATE: 1997-05-23 ; EARLIER APPLICATION NUMBER: 60/047,632
δλ	173 GATACATCACAGACTCATACAAA	; EARLIER FILING DATE: 1997-05-23 ; EARLIER APPLICATION NUMBER: 60/047,601
ପୁପ	1866 GATACATCACAGACTCATACAAA 1888	FILING DATE: 1997-09
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
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EARLIER APPLICATION NUMBER: 60/043,314

RESULT 12 US-09-148-545-21 ; Sequence 21, Application US/09148545 ; Patent No. 6590075

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EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,662
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APPLICATION NUMBER: 60/056,877
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347 AGGAGCTGGCCGTGCGACTGGGCTTTCGGGCCCTGTG-CAGAGGAGCAGCCTTCCTGAG 6 AGGAGCTGGCCGTCCACTCGGCCTTCGGGCCCTGTGCCAGAGGAGCANGCCTTCCTGAG 466 GCAGGAGGATGAGTCCCAGTGGTAGCTATTATGGCCACTGGTGGTGGATCCGGGCAAT GACTICCCTGIAIGGCAGCIGGCIGGCTGAAGGAGCIGGGCCICTIGGAITGCGICIC 186 GACTICCCTGTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCTCTTGGATTGCKTCTC 35; Gaps DB 4; Length 1926; 4; Indels Query Match

80.7%; Score 1777.8;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1844; Conservative 1; Mismatches EARLIER APPLICATION NUMBER: 60/047,588
BARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION UNMERS: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22 ER FILING DATE: 1997-08-22
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ER PILING DATE: 1997-08-22
ER PILING DATE: 1997-08-22
ER PILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,889
ER PILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,880
ER PILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,894 ER FILING DATE: 1997-08-27

ER APPLICATION NUMBER: 60/056,911

ER PILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,636

ER PILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,814

ER APPLICATION NUMBER: 60/056,910

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,84

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ER PILING DATE: 1997-08-22

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ER PILING DATE: 05-SEP-1997 TR APPLICATION NUMBER: 60/043,578
TR FILING DATE: 1997-04-11
TR APPLICATION NUMBER: 60/043,576
TR FILING DATE: 1997-04-11
TR APPLICATION NUMBER: 60/047,501
TR APPLICATION NUMBER: 60/047,501
TR APPLICATION NUMBER: 60/043,670
TR APPLICATION NUMBER: 60/043,670
TR FILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/047,585
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,590
R FILING DATE: 1997-05-23 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,878 APPLICATION NUMBER: 60/047,594 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,589 APPLICATION NUMBER: 60/047,593 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,614 FILING DATE: 1997-05-23 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 APPLICATION NUMBER: 60/056,664 FILING DATE: 1997-05-23 EARLIER 1 EARLIER 1 EARLIER 1 EARLIER EARLIER EARLIER EARLIER DEAR EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER DEAR EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER

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Pred. No. 0;
3; Mismatches
         EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER PILING DATE: 1997-08-22
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Matches 1745; Conserv
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Sequence 1, Application US/08827208
Patent No. 6025178
GENERAL INFORMATION,
APPLICANT: Kramer, Ruth M.
APPLICANT: Pickard, Richard T.
APPLICANT: Striffer, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: US 60/014,608
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTONNEV AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: x-10610
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/827,208
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
                                                                                                                                               ....urESSEE: Bli Lilly and Company STREET: Lilly Corporate Center STATE: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 8517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 79.3
Matches 1957; Conservative
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7473..8499
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ADDRESSEE: Eli Lilly
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6225 GGCCGCGCGCCTTGACCCAGGCCCTGCAGCTGGAGAGACCTGCAGGAGATGAGATACC 6284
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244 GGCTGGAGTGCAATGGCGTGATCTTGGCTCACTGCAACCTCCGCCTCTGGGGTTCAAGCG 303
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                        6045 GGCTGGAGTGCAATGGCGTGATCTTGGCTCACTGCAACCTCCGCCTCTGGGGTTCAAGCG
                                                                                                                              6105 ATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGACTGAGGGAGCTGGCCGTGCG
                                                                                                                                                                                                                     6165 ACTGGGCTTCGGGCCCTGTGCAGAGAGAGCAGCCTTCCTGAGCAGGAGGAGGAGGTGGT
                                                                                                                                                                                     ACTOGGCCTTCGGGCCCTGTGCAGAGGAGCAGCCTTCCTGAGCAGGAGGAAGCAGGTGGT
                                                                                       304 ATTCTCCTCCTCAGCCTCCCGAGTAGCTGGGATTACAGACTGAGGGAGCTGGCGGTGCG
                                                                                                                                                                                                                                                                                 GGCCGCGCGCCCTTGAGGCCCCTGCAGCTGGAGGACCTGCAGGAGGATGAGAT-CC
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DECEMBER DECEMBER	COMPUTER: IEM PC compatible COMPUTER: IEM PC compatible COMPUTER: IEM PC compatible CURRENT APPLICATION DATA: PRICE APPLICATION DATA: PRICE APPLICATION DATA: PRICE APPLICATION DATA: APPLICATION NUMBER: US/08/827,208 FILING DATE: 28-WAR-1997 FILING DATE: 29-WAR-1997 FILING DATE: 29-WAR-1997 FILING DATE: 29-WAR-1997 FILING DATE: 19-WAR-1997 FILIN
	1571 TGCCAGGAGCAGCACTCCACCATTCCACCAGTTGCAGCTCCTGGGCCGGTTC

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MOLECULE TYPE: DNA (genomic)	Query Quer	

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CCCGGAGCCCTGCGGTGCTGCAC 1690		GCCCTGGGGTCCGGCGGACACCC 8024				scrécaccreacarracaarere 8144		czadaczackackackak		cccreccacccraacrcrcarrcarrccreecr 8264		CTTCAGAGCCTCGGGCTCAGGTGGC 8324		CCTTGCGCCTCAGCAGTTTGCAGTG 8384		AAAACCCCCCGGCCTGTGCCTGTTT 8444		GATACATCACAGACTCATACAAAA 8504			
CCTCGGGAGTGCCACCTTCTCCGACCCCACCTGCCCGGAGCCCCTGCGGTGCTGCACCCTGCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG		 TTTCCTCTGGTCAGCGACTCCTTCCGGGAGTACTCGGCCCCTGGGGGTCCGGCGGACACCC	GAGGAGGCGGCAGCTGGGGAGGTGAACCTGTCTTCATCGGACT	GAGGAGGCGGCAGCTGGGGAGGTGAACCTGTCTTCATCGGACTCTCCCTACCACTACACG	AAGGTGACCTACAGCCAGGAGGACGTGGACAAGCTGCTGCACCTGACACATTACAATGTC	AAGGTGACCTACAGCCAGGAGGACGTGGACAAGCTGCTGCACACATTACAATGTC		TGCAACAACCAGGAGCTGCTGGAGGCTCTGCGCCAGGCAGTGCAGCGGAGGCGGCAG	CGCAGGCCCCACTGATGGCCGGGGC	CGCAGGCCCCACTGATGGCCGGGGC		GCTGAGTTGCAGGTGGGAACTGTCATCACGCAGTGCTTCAGAGCCTCGGGCTCAGGTGGC		; Acedroccaedaricoadecreadecregedecocorrecercaecaetrocaere		. GGGTAAGGGGCCAAGCCCATTTGTGTATCACCCAAAACCCCCGGCCTGTGTTT	3 TCCCTTCTGCGCTACCTTGAGTAGGTGGAGCACTTGATACATCACAGACTCATACAAAA	: TCCCTTCTGCGCTACCTTGAGTAGTTGGAGCACTTGATACAT	3 AAAAAAA 2204	5 AAAAAA 8511	
1631	1691	7965	1718	8025	1778	8085	1838	8145	1898	8205	1958	8265	2018	8325	2078	8385	2138	8445	2198	8505	
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Search completed: October 7, 2004, 18:59:56 Job time: 208.207 secs

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Sequence 3, Application US/10266388 Publication No. US20030124702A1 GENERAL INFORMATION:
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Sequence 81, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 87, Appl
Sequence 127, Appl
Sequence 127, Appl
Sequence 127, Appl
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Sequence 2564, Appl
Sequence 27, Appl
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Sequence 1, Appli
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-918-995-32564
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US-10-380-873B-2
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US-10-332-426-14
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                                                             OM nucleic - nucleic search, using sw model
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US-10-380-873B-39		US-09-918-995-28234	6	US-10-296-115-1	US-10-380-873B-4				US-10-444-795B-R08					US-10-079-854-372	7		TIS-10-087-192-136	US-10-052-482-1	115-10-085-117-3		US-10-183-7/0-3	TIS-10-741-601-1214E	TIG-10-027-632 25143	TR-10-027-632-232430	US-09-805-456-3			US-10-225-810-26		US-10-027-632-
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365	358.6	235.6	172.4	166.6	150	136.8	136.8	132.8	131.8	131.8	131.8	130.8	130.6	130.6	130.4	130.2	130.2	129.8	129.8	129.8	129.8	129.6	129.6	129.6	129.6	129.6	129.6	129.6	129.4	129.4
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ALIGNMENTS

APPLICANT: Kriz, Ron Song, Chuanzheng TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge

COMPUTER READABLE FORM: COUNTRY: USA ZIP: 02140 STATE: MA

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/266,388
FILING DATE: 07-Oct-2002
CLASSIFICATION: <Unknown>
RPLICATION DATA:
APPLICATION NUMBER: US/09/895,547
FILING DATE: 29-Jun-2001
APPLICATION NUMBER: 09/460,145

NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724 REFERENCE/DOCKET NUMBER: G15289

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

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RESULT 2
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; JENGTH: 2699 Dase pairs
; TYPE: nucleic acid
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                                            Song, Chuanzheng
Song, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4183;
                                                                                                                                                                                                      MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/266,388
FILING DATE: 07-Oct-2002
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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APPLICATION NUMBER: US/09/895,547
FILING DATE: 29-Unn-2001
APPLICATION NUMBER: 09/460,145
FILING DATE: «UNKNOWN:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.0%; Score 1806.2;
98.1%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI5289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ 1D NO: 1:
US-10-266-388-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4183 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
Publication No. US20030124702A1
GENERAL INFORMATION:
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                              APPLICANT: Kriz, Ron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.1
Matches 1851; Conservative
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ZIP: 02140
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PRIOR APPLICATION NUMBER: 60/047,613
PRIOR FILING DATE: 1997-05-23
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PRIOR FILING DATE: 1997-05-23
PRIOR PELICATION NUMBER: 60/047,612
PRIOR FILING DATE: 1997-05-23
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APPLICATION WUMBER: 60/056,872
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,882
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,581
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,587
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                         FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
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                                                                     AGCTGCTGCACCTGACACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTC 1868
                                                                                                                                                                                                                                                                                        3912
3733 CITCAICGGACICTCCCIACCACIACAGGAGGIGACCIACAGCCAGGAGGACGIGGACA 3792
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                                                                                                                                                                                                                                                              1869 TGCGCCAGGCAGTGCAGCGGAGGCGGCAGCGCCCCCACTGATGGCCGGGGCCCCTGC
                                                                                                                                                                                                                                                                                                                                                             CACCCCTAACTCTCATTCCTTGGCTGCTGAGTTGCAGGTGGGAACTGTCATCACGC
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                                                                                                                           3793 AGCIGCIGCACCIGACACATTACAAIGTCTGCAACAACCAGGAGCAGCIGCIGGAGGGGGGGCTG
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APPLICATION NUMBER: 60/047,617
FILING DATE: 1997-05-23
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Patent No. US20020164669A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/056,631
PRIOR APPLICATION NUMBER: 60/056,845
PRIOR APPLICATION NUMBER: 60/056,845
PRIOR APPLICATION NUMBER: 60/056,892
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-06-23
PRIOR PLING DATE: 1997-05-23
PRIOR PLING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,595
PRIOR PLING DATE: 05-Sep-1997
PRIOR APPLICATION NUMBER: 60/047,599
PRIOR FILING DATE: 1997-05-23
PRIOR PLING DATE: 1997-05-23
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,636
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,637
                                                 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,903
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APPLICATION NUMBER: 60/056,888
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,879
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APPLICATION NUMBER: 60/056,874
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APPLICATION NUMBER: 60/056,910
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,631
FILING DATE: 1997-08-22
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405 1005 465 125 525 185 585 245 645 1006 CITCAICCCCICTGAGCICTIIGGCTCCGAGTICTITAIGGGGCAGCIGAIGAAGAGGCT 1065 TCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCAACCT 1125 CCAGGACAGCITAIACTGGGCCTCAGAGCCCAGCAGTTCTGGGACCGCTCGGTCAGGAA 1185 705 765 425 485 885 65 945 605 347 AGGGAGCTGGCCGTGCGACTGGGGCTTCGGGCCCTGTG-CAGAGGAGCAGCCTTCCTGAG 466 GCAGAAGATGAGATCCCAGTGGTAGTTATGCCCACTGGTGGTGGATCCGGGCAAT 526 GACTICCCTGTATGGGCAGCTGGCTGAAGGAGCTGGGCCTCTTGGATTGCGTCTC CTACATCACCGGGGCCTCGGGCTCCACCTGGGCCTTGGCCAACCTTTATGAGGACCCAGA GTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGAAGACCCCAGGTGACCAAGAA CAAGCTGGGTGTGCTGGCCCCCAGCTGCAGCTGCGGGTACCGGCAGGAGCTGGCCGAGCG 946 TGAATTTGGGGAGTGGTGCGAGTTCTCTCTCTACGAGGTCGGGTTCCCCAAGTACGGGGC TGCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGGCCCTCATCAACGAGGCGCT 826 GCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAAGGCCCTGAGTCATGG 486 GCTGCATGATGAGCCCCCATGATCACAGAGCTCTCAGATCAACGGGAGGCCCTGAGTCATGG Gaps 726 TCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCAACCT 34; DB 9; Length 1925, 4; Indels Score 1788.8; Pred. No. 0; 1; Mismatches PRIOR APPLICATION NUMBER: 60/056,887
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,908
PRIOR APPLICATION NUMBER: 60/046,964
PRIOR PLING DATE: 1997-08-22
PRIOR PLLING DATE: 1997-06-66
PRIOR PLLING DATE: 1997-06-67
PRIOR PLLING DATE: 1997-09-05
PRIOR PLLING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SEQ ID NO 86
TENGTH: 1925 81.2%; 97.9%; Query Match Best Local Similarity 97.9; Matches 1844; Conservative 186 586 246 646 306 904 999 9901 1126 à 원 ò du ò 셤 à g à g à g g ⋧ à g g ઠે ð 임 ò 엄 ò g ð d

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APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1
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CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1998-03-07
EARLIER FILING DATE: 1997-03-07
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APPLICATION WUMBER: 60/047,632
APPLICATION WUMBER: 60/047,601
APPLICATION NUMBER: 60/047,601
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,618
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APPLICATION NUMBER: 60/047,581
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APPLICATION NUMBER: 60/047,583
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,615
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APPLICATION NUMBER: 60/047,600
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APPLICATION NUMBER: 60/047,597
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APPLICATION NUMBER: 60/047,502
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APPLICATION NUMBER: 60/040,336
                                                                                       Sequence 86, Application US/09148545
Publication No. US20030027132A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/043,569
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,311
                      60/043,580
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APPLICATION NUMBER: 60/043,568
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APPLICATION NUMBER: 60/043,314
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APPLICATION NUMBER: 60/043,672
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APPLICATION NUMBER: 60/043,671
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APPLICATION NUMBER: 60/048,974
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APPLICATION NUMBER: 60/056,630
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APPLICATION NUMBER: 60/056,886
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APPLICATION NUMBER: 60/056,877
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APPLICATION NUMBER: 60/056,893
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APPLICATION NUMBER: 60/056,878
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APPLICATION NUMBER: 60/056,662
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APPLICATION NUMBER: 60/056,910
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APPLICATION NUMBER: 60/056,892
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APPLICATION NUMBER: 60/056,881 EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
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Pred. No. 0;
1; Mismatches
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/056,632
PRIOR FILING DATE: 1997-08-22
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EBARLIER APPLICATION NUMBER: 60/047,613
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EBARLIER FILING DATE: 1997-05-23
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EBARLIER APPLICATION NUMBER: 60/043,580
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R APPLICATION NUMBER: 60/056,882
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APPLICATION NUMBER: 60/056,886
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Publication No. US20030027132A1
GRNEAT INCOMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT PAPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER APLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1998-03-07
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186 CCAGGACAGCTTATACTGGGCCTCAGAGCCCAGCTGTCTGGGACCGCTGGGTCAGGAA 1006 CITCATCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGGCT TCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCAACCTGTATGCAGCCAACCT 666 CITCAICCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGGGGCAGCTGATGAAGAGCT CTACATCACCGGGGCTCCGGCCTCGGGCCTTGGCCAACCTTTATGAGGACCCAGA 646 gragicicacaagaaccragcagacccacragragragragragaaccaagagaaccaagaa 306 GIGGICTCAGAAGGACCIGGCAGGCCCACIGAGTIGCIGAAGACCCAGGIGACCAAGAA CAAGCTGGGTGTGGTGGCCCCCCAGCTGCAGCGGTACCGGCAGGAGCTGGCCGAGCG TGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCCTCATCAACGAGGCGCT GACTTCCCTCTATGGGCAGCTGGCTGGCCTGAAGGAGCTGGGCTCTTGGATTGCGTTTC GACTICCCTGTATGGGCAGCTGGCTGGCTGGAAGAGAGTGGGCCTCTTGGATTGCKTCTC 347 AGGGAGCTGGCCGTGCGACTTCGGGCCCTGTG-CAGAGGAGCAGGCCTTCCTGAG 6 AGGGAGCTGGCCGTGCGACTGGGCTTCGGGCCCTGTGCCCAGGGAGGAGCANGCCTTCCTGAG 35; Gaps DB 10; Length 1926; Indels 4; Score 1777.8; Pred. No. 0; 1; Mismatches Query Match Best Local Similarity 97.9%; Matches 1844; Conservative 1126 1186 846 906 1306 9901 996 991 826 486 904 99 466 126 526 186 586 246 셤 g g à 엄 à g à 8 g ò 원 à g $\overset{\circ}{\circ}$ g ò g ò ò 셤 à 원 à qq g ò g 8 8 Db δ à

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PRIOR APPLICATION NUMBER: 60/040,333
PRIOR PILING DATE: 1997-03-07
PRIOR PELICATION NUMBER: 60/040,333
PRIOR PLILNG DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,625
PRIOR PELING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,161
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Patent No. US20020164669A1
FABERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/148,545
PRIOR FILING DATE: 1998-09-04
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76.1%; Score 1676.6;

Best Local Similarity 97.4%; Pred. No. 0;

Matches 1745; Conservative 3; Mismatches PRIOR APPLICATION NUMBER: 60/047,589
PRIOR APPLICATION NUMBER: 60/047,589
PRIOR FILING DATE: 1997-05-23
PRIOR FILING DATE: 1997-05-23
PRIOR FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/056,894
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EARLIER PILING DATE: 1997-08-22
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; Publication No. US20040029136A1
; GENERAL INPORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom;
; APPLICANT: THORNTON, Michael; LU, Dyung Alna M.;
; APPLICANT: TRIBOULEY, Catherine M.; YUE, Henry;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.;
; APPLICANT: YAO, Monique G.; HAPALIA, April J. A.;
; APPLICANT: ELLIOTT, Vicki S.; ARVIZU, Chandra S.;
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Pred. No. 0;
3; Mismatches
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 87
                                                                                             Query Match
Best Local Similarity 97.4%;
Matches 1745; Conservative
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US-10-332-426-14
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Pred. No. 5.4e-152;
0; Mismatches 565; Indels
                              APPLICANT: LAL, Preeti; RAMKUMAR, Jayalaxmi;
APPLICANT: NGUYEN, Danniel B.; BAUGHN, Mariah R.
TITLE OF INVENTION: LIPID METABOLISM MOLECULES
TITLE OF INVENTION: LIPID METABOLISM MOLECULES
TILLE OF INVENTION DATE: 2000
CURRENT FILING DATE: 2003-61-66
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,803
PRIOR APPLICATION NUMBER: US 60/216,801
PRIOR APPLICATION NUMBER: US 60/218,233
PRIOR APPLICATION NUMBER: US 60/218,233
PRIOR FILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-26
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PRIOR APPLICATION NUMBER: US 60/220,739
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SOFTWARE: PERL PROGRAM
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          Sequence 127, Application US/10103313
Publication No. US20030082758A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: DV207C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
FPIOR Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 127
LENGTH: 1915
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE REFERENCE: 2011-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                        22.0%; Score 483.8; DB 15
98.4%; Pred. No. 3.8e-120;
tive 0; Mismatches 7;
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Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     Best Local Similarity 98.4 Matches 499; Conservative
                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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US-10-103-313-127
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Publication No. US20040086905A1

GENERAL INFORMATION:

APPLICANT: DAS. Deborrya; YAO, Monique G.;

APPLICANT: ARVIZU, Chandra S.; BAUGHN, Mariah R.;

APPLICANT: LU, Yan; HAFALIA, April J.A.;

APPLICANT: LU, Dyung Alina M.; YUE, Henry;

APPLICANT: DINO, Li; ELLIOTT, Vicki S.;

APPLICANT: GRSYTHE, Ian J.; RAMKUMAR, Jayalaxmi;

APPLICANT: GANDHI, Ameena R.; ISON, Craig H.;

APPLICANT: GANDHI, Ameena R.; TANG, Y. Tom;

APPLICANT: EMERING, Bridget A.; TANG, Y. Tom;

APPLICANT: TEMELING, Brooke M.; HONCHELL, Cynthia D.;

APPLICANT: TYNE Michael: Barbooch
                                                                                                                                                                                                                                                                                                                            Score 439; DB 10;
Pred. No. 3.4e-108;
0; Mismatches 7;
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TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
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NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32564
LENGTH: 494
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CURRENT APPLICATION NUMBER: US/10/467,248
CURRENT FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: PCT/US02/03813
PRIOR FILING DATE: 2002-02-06
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-06
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                                                                                                                                                                                                                     ; LOCATION: (1). T. (494)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32564
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.4%;
Matches 442; Conservative
                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                    NAME/KEY: misc_feature
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1345

1465 2814

us-09-830-321a-5.rnpb

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GAAGAGCAGCTCCAGCCTCGGGAGTGCCACGTTCTCCGACCCCACCTGCCCGGAGCC 1675
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TITLE OF INVENTION: POLYPEPtide having phospholipase A2 activity
FILE REFERENCE: 2139.34
CURRENT APPLICATION NUMBER: US/10/380,873B
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: JP 00/146466
PRIOR FILING DATE: 2000-09-19
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US-10-380-873B-2
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Pred. No. 1.9e-105;
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OTHER INFORMATION: Incyte ID No: 7472774CB1
                                       PRIOR APPLICATION NUMBER: US 60/276,891
PRIOR FILING DATE: 2001-03-16
PRIOR PLILORION NUMBER: US 60/276,855
PRIOR PLILNG DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR PLICATION NUMBER: US 60/283,818
PRIOR PLILOGATION NUMBER: US 60/283,818
PRIOR PLILOGATION NUMBER: US 60/285,405
PRIOR PLILOR DATE: 2001-04-13
PRIOR PLILNG DATE: 2001-04-20
PRIOR PLILNG DATE: 2001-04-20
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Best Local Similarity 56.2%;
Matches 909; Conservative
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APPLICANT: AZIMZAI, Yalda; DAS, Debopriya;
APPLICANT: TROPRYON, Michael; Ju, Dyung Aina M.;
APPLICANT: TRIBOULEY, Catherine M.; YuE, Henry;
APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.;
APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.;
APPLICANT: KHAN, Farrah A.; Lu, Yan;
APPLICANT: ELLIOTT, Vicki S.; ARVIZU, Chandra S.;
APPLICANT: Lal, Preeti; RAMKUMAR, Jayalaxmi;
APPLICANT: Lal, Preeti; RAMKUMAR, Jayalaxmi;
APPLICANT: MUSTEN, Danniel B.; BAUGHN, Mariah R.;
TITLE OF INVENTION: LIPID METABOLISM MOLECULES
FILE REFERENCE: PI-0152 USN
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CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: US 60/216,803
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Publication No. US20040029136A1
GENERAL INFORMATION:
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Best Local Similarity 55.2%; Pred. No. 5.5e-97;
Matches 880; Conservative 0; Mismatches 658; Indels
       01/284044
PRIOR APPLICATION NUMBER: JP (
PRIOR FILING DATE: 2001-05-16
                                        NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 3460
                                                                                                                                  ; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

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TITLE OF INVENTION: Polypeptide having phospholipase A2 activity
FILE REFERENCE: 2139.34
CURRENT APPLICATION NUMBER: US/10/380,873B
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: JP 00/146466
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; OTHER INFORMATION: Incyte ID No. US20040029136A1 1281946CB1
US-10-332-426-11
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Pred. No. 1.1e-93;
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,801
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR PLILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/220,046
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-26
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PRIOR FILING DATE: 2000-07-6
PRIOR FILING DATE: 2000-07-6
PRIOR FILING DATE: 2000-07-6
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 16
SOCYTARRE: PERL PROGRAM
SEQ ID NO 11
LENGTH: 2547
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Best Local Similarity 54.7%;
Matches 873; Conservative
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Job time : 1150.17 secs
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                                                                                                                                                                                                                                                                                                                                    Score 365; DB 16; Length 2694;
Pred. No. 4.7e-88;
0; Mismatches 665; Indels 78
PRIOR FILING DATE: 2000-09-19
PRIOR PEDLICATION NUMBER: JP 01/284044
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 47
SCFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
LENGTH: 2694
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Best Local Similarity 54.3%;
Matches 882; Conservative
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; NAME/KEY: CDS
; LOCATION: (52)...(2610)
US-10-380-873B-39
                                                                                                                                                               TYPE: DNA ORGANISM: Mus musculus
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Canome Res. 10 (10), 1617-1630 (2000)
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Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched library, clone:A030011C02 product:similar to CYTOSOLIC PAOSPHOLIPASE A2 BETA [Homo sapiens], full insert sequence.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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CA319426
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Minimum DB Maximum DB

Database

Searched:

HTC 19-SEP-2003

No. Result

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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-resegges.riken.go.jp,
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Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                           The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length OnNAs
Nature 420, 563-573 (2002)
6 (bases I to 4240)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Indrahl, K., Ishi, Y., Itoh, M., Kagawa, T., Hirozane, T., Hori, F., Inotahl, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamira, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tomaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Yasunishi, F., Takahira, S.,
              Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Skonno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Indue, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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Pred. No. 1.3e-215;
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URL:http://fantom.gsc.riken.go.jp/
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Nature 409, 685-690 (2001)
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1467 GCTGCCCTGCCCTGCAGCCCACTCGGGACGTGGACC-TCATCCTGTCATTGGACTAC 1525
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Pred. No. 3.8e-168;
0; Mismatches 60;
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Best Local Similarity 93.4%;
Matches 998; Conservative (
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
El (bases I to 1131)

NHH-MGC http://mgc.nci.nih.gov/.
NHT-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
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CDNA Library Argaed by: The I.M.A.G.E. Consortium (LIML)
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Plate: LLAMI2832 row: j column: 18
High quality sequence stop: 629.

Location/Qualifiers

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         1473
                                                      1474 GCCCCTCCTGCAGCCCACTCGGGACGTGGACCTCATCCTGTCATTGGACTACAACCTCCA 1533
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BM928260.1 GI:19378639
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: ECGRV (destroyed); RNA source anonymous pool of 3 feta_1 brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (ECGRV site is destroyed upon 0.7-3: Skb Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

9 1046 1106 1166 989 746 1226 1286 1346 1406 137 908 197 866 257 926 317 986 437 497 17 557 617 677 737 797 ACCTITATGAGGACCCAGAGTGGTCTCAGAAGGACCTGGCAGGGCCCACTGAGTTGCTGA 747 GGCAGGAGCTGGCCGAGCGTGCCCGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGG CCCTCATCAACGAGGCGCTGCTGCATGATGAGCCCCATGATCACAAGCTCTCAGATCAAC GGGAGGCCCTGAGTCATGGCCAGAACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAG GGCAGAGCCTGACCACTTTTGAATTTGGGGGAGTGGTGCGAGTTCTCCTCCCTACGAGGTCG GCTTCCCCAAGTACGGGGCCTTCATCCCCTCTGAGCTCTTTGGCTCCGAGTTCTTTATGG 1047 GGCAGCTGATGAAGAGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCA 438 GGCAGCTGATGAAGAGGCTTCCTGAGTCCCGCATCTGCTTCTTAGAAGGTATCTGGAGCA 1167 GGGACCGCTGGGTCAGGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGA 1347 ACTITICAGCATCCTCACTTCTCCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACC 1287 GGCGTCCACTGGCCCAGGCCACATAATTTCCTGCGTGGCCTCCATTTCCACAAAGACT Gaps 1227 TAGAAGAACCACCTCAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGT 678 GGCGTCCACTCGCCCAGGCCACACATATTTCCTGCGTGGCGCTCATTTTCCACAGACT 60; Indels

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BI768993 949 bp mRNA linear EST 25-SEP-2001 603058145F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207531 5', mRNA sequence.
BI768993
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NIH-MGC http://wgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
L Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Mor Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llhi.gov
Plate: LiAM11520 row: j column: 12
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 949)
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522 CAATGACTTCCCTGTATGGGCAGCTGGCCTGGCAGGAGCTGGGCCTCTTGGATTGCG
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(Dases 1 to 957)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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            Gaps
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

feund through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14278 row: I column: 17
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                                                                                                                                                                                                                                         1636 gangrecchecerrecencecececerecedadececeracearg 1684
                                                                                                                                                                                                                                                                          1038 GAAGGCCCACCCTTTTTTGACCCACCTGGCCCCGGAAACCCCCTGGG 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Homo sapiens"
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Location/Qualifiers
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'db xref="taxon:9606"
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/tissue_type="Lung"
/tissue_type="Lung"
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/lab_bost="Plang (Life Technologies) (TI phage resistant)"
/lab_bost="Plang (Life Technologies) (TI phage resistant)"
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/clone lib="UI-CR-ECI"
/mote="Torgan: Lung; Vector: pT773-pac (Pharmacia) with a modified polyluiker; Site 1: Scok I; Site 2: Not I;
UI-CR-ECI is a normalized CDNA library containing the following tissue(8): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into PT713-Pac vector. The oligonucleotide used to prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7771
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayded by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BU688449 17-0-UI.59 bp mRNA linear EST 07-0CT-2002 UI-CF-EC1-aea-j-17-0-UI.51 UI-CF-EC1 Homo sapiens cDNA clone UI-CF-EC1.aea-j-17-0-UI 3', mRNA sequence.
                                                                                                                           1768 CCACTACACG-AAGGTGACCTACAGCCAGGAGG---ACGTGGACAAGCTGCTGGACTGA 1823
                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 759)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                   1711 GACA-CCCGAGGAGGCGGCAGCTGGAGGTGAACCTGT--CTTCATCGGACTCTCCTA
                                                  1824 CACATTACAATGTCTGCAACAACCAGGAGCAGCTGCTGGAGGCTCTGCGCCAGGCAGTGC
                                                                                                                                                                             780 CCACTACACGAAATGTGACTTACAGCCAGAGGGACCGTGGGACCAAGCTGTGCACTGAA
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BM718675 647 bp mRNA linear BST 01-MAR-2002 UI-E-E01-ajc-i-21-0-UI.rl UI-E-E01 Homo sapiens cDNA clone UI-E-E01-ajc-i-21-0-UI 5', mRNA sequence.

DEFINITION

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/db xret="taxxon:9bub"
/dlone="ul_E-BCD1-ajc-i-21-0-UI"
/tissue type="fetal eye"
/dev_stage="fetal"
/lab_host="mthins (inife Technologies) (T1 phage resistant)"
/lab_host="mthins (inife Technologies) (T1 phage resistant)"
/clone lib="ul-E-BCD"
/note="organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR 1; Site 2: Not I;
ul-E-BCD is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an ECoR I
adaptor, digested with Not I, and cloned directionally
into pT713-pac vector: The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGGGTATACC. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI)."
                                                                                                                                                                                                                                                                                                                               Coordinated Laboratory for Computational Genomics
University of Iowa
University of Iowa
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
761: 319 315 8250
Fax: 319 315 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
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                                           Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1 (bases 1 to 647)]
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Pred. No. 3.5e-116;
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97044477
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/db_xref="taxon:9606"
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Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                         Contact: Soares, MB
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2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Eax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.researcher) or from Open Blosystems
TCTCAGAAGGACCTGGCAGGCCCACTGAGTTGCTGAAGACCCAGGTGACCAAGAACAAG 240
                                                                            300
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                                                                                                                           301 CGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCTCATCAATGAGGCGCTGCTG 360
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Bonaldo,M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                   CGCTTGGGCTACCCAAGCTGCTTCACCAACCTGTGGGCCCCTCATCAACGAGGCGCTGCTG
                                                                                                                                                                        CATGATGAGCCCCATGATCACAAGCTCTCAGATCAACGGGAGGCCCTGAGTCATGGCCAG
                                                                                                                                                                                            AACCCTCTGCCCATCTACTGTGCCCTCAACACCAAAGGGCAGAGCCTGACCACTTTTGAA
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/tissue_type="Primary Lung Cystic Fibrosis Epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1070 GAGTCCCGCATCTGCTTAGAAGGTATCTGGAGCAAC 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGTCTCGCATCTGCTTCTTANAAGGTATCTGGAGCACC 639
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Seq primer: M13 FORWARD
POLYA=Yes.
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BM982475/c
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TITLE
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PUBMED
COMMENT
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/note="Organ: Lucr-can."
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//dev stage="Adult"
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//clone lib="UT-CF-EN1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.9%; Score 615.2; DB 12; Length 701; 94.7%; Pred. No. 1.4e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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TAG LIB=UI-CF-EN1
TAG SEQ=CTGCTCAGGT"
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BG686408 1inear EST 07-MAY-2001 602659504F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802713 5',
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                                                                                                                                                                                                                    1239 CCTCAACAGCCGGCAGAATAGCTGAGTTTTTCACCGATCTTCTGACGTGGCGTCCACTGG 1298
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/ste_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 935)
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Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llhl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 CGGAGCCCCACTGTGCCTGCTGGATGTTGGCTACCTCATCAATAACCAGCTGCCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCACITICICCACATGGAAAGCTACCACTCTGGATGGGCTCCCCAACCAGCTGACACCT
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                                                                                               1179 TCAGGAACCAGGCCAACCTGGACAAGGAGCAGGTCCCCCTTCTGAAGAAGAAGAACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Rml0A07 Betheada, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

CDNA Library Preparation: Information Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.lln.gov

Righ quality sequence start: 6

High quality sequence start: 6

High quality sequence store: 549.
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( Dases 1 to 869)

NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                      organism="Homo sapiens"
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g ð Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Bases 1 to 1149)

E 1 (Bases 1 to 1149)

NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Library Library Arrayed by: Agencourt Bioscience Loropration

Clone Library Arrayed by: Agencourt Bioscience Loropration

Clone Library Arrayed by: Agencourt Bioscience Corporation

Clone Library Arrayed by: Agencourt Bioscience Corporation

Clound through the I.M.A.G.E. Consortium/Library

Plate: Library Arrayed by: Agencourt Bioscience Corporation

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Plate: Library Arrayed by: Agencourt Bioscience Corporation

Cloud through the I.M.A.G.E. Column: 09

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Homo sapiens

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/lab.host="DMINGS"
/clone lib="NIH MGC 125"
/clone lib="NIH MGC 125"
/clone lib="NIH MGC 125"
/note="Corgan: ovary' (pool of 3); Vector: pCMV-SPORT6;
Site l: EcoRV (destroyed); Site 2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to of three ovaries, from females ranging in age from 38 to of three ovaries is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2:1 kb, insert size range 1-3:5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

/organism="Homo sapiens"

/mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5590352"

High quality sequence stop: 568 Location/Qualifiers

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  26.1%; Score 574.4; DB 12; Length 1149; 92.0%; Pred. No. 2e-104;
                          21; Indels
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            Similarity
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AGENCOURT_6620095 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590352 5', mRNA sequence.
BM906397.1 GI:19356776
EST.

LOCUS DEFINITION RESULT 10 BM906397

ACCESSION VERSION KEYWORDS Gene Eye

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922 bp mRNA linear EST 16-AUG-2002 AGENCOURT 8764474 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6312998 5', mRNA Sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
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sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, GE Discovery in the Visual System, supported by National By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1796 GAGGACGTGGAGGTGCTGCTGCACCTGACATTACAATGTCTGCAACAACCAGGAGCAG
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Pred, No. 1.7e-103;
0; Mismatches 2;
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TAG TISSUE=human fetal eye
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TAG_SEQ=CGCGTATACC"
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UI-B-EO1-ajc-i-21-0-UI.sl UI-B-EO1 Homo sapiens CDNA clone
UI-B-EO1-ajc-i-21-0-UI 3', mRNA sequence.
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Coordinated Laboratory for Computational Genomics
University of Iowa
University of Iowa
Tel: 319 335 9856
Fax: 319 335 9856
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Seg primer: M13 FORWARD
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                                                                                                                                                                                                                                                                                    mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
                                                                                            1275 ATCTTCTGACGTGGGGTCCACTGGCCCAGGCCACATAATTTCCTGCGTGGCCTCCATT
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                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 666)
Hegde,P., (Ji.R., Abernathy.K., Dharap,S., Gaspard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

25.3%; Score 558.2; DB 10; Length 666;
Best Local Similarity 92.0%; Pred. No. 3.6e-101;
Matches 612; Conservative 0; Mismatches 20; Indels 33;
                                                                                                                                                                                                                                                              AW959903 666 bp mRNA linear EST371974 MAGE resequences, MAGF Homo sapiens CDNA,
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                       CCATTICCACAAAGACTACTICAGCAICCICACTICICCAC 1371
                                                                                                                                                                      CCATTTCCACAAAGGACTATTTCAGAAACTCTCAACTTCTC 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol type="mRNA"
/db xzef="taxon:9606"
/clone lib="MAGE resequences, MAGF"
/note="Vector: pBluescriptsKm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                               AW959903.1 GI:8149587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: johnq@tigr.org
Plate: 139
                                                                                                                                                                                                                                                                                                                                                     sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: Reverse
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VERSION
KEYWORDS
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AW959903
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                                                                                                                                                                                                                                                                                                                                   /lab_host="DHIOB (phage-resistant)"
/clone lib="NNH MGC 129"
/note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
Site_1: EcoRV; Site_2: Not1; Cloned unidirectionally.
By Reset oligo dT. Average insert size 2.2 kb. Constructed by Resegen, Invitrogen Corp. Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Found through the I.M.A.G.E. Consortium/LLNL at:
High quality sequence stop: 622.
High quality sequence stop: 622.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 562; DB 13; Length 922;
Pred. No. 6.2e-102;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                 1. .922
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6312998"
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with EcoR I adaptor, digested with NotI and then cloned directionally into pxx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGACACAG. This library was created for the University lows Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1129 GGACAGCTTATACTGGGCCTCAGAGCCCAGCCAGTTCTGGGACCGCTGGGTCAGGAACCA 1188
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                                                                                                                                                                                                                                                                                                                       DB 14; Length 810;
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                                                                                                                                                                                                                                                                                                                             Score 556.2; DB 14;
Pred. No. 9e-101;
0; Mismatches 138;
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UI-M-FW0-cbz-n-15-0-UI.rl NIH_BMAP_FW0 Mus musculus cDNA clone
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                                               AGGAGCAGGGGATCCCGTTCCCACCCATCTCGCCCAGCCCCGAAGAGCAGCTCCAGCTC 360
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 910)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE: 6816688 5', mRNA sequence
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/strain="C57BL/6"
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JOURNAL
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Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 579)
Dias Neto, E. Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
  BF769253
QV3-IT00008-111100-413-c05 IT0008 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.bz/scripts/gethtml2.pl?tl=QV3&t2=QV3-IT0008-111100-413-C05&t3=2000-11-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev stage="Adult"
/clone lib="IT0008"
/note="Corgan: epid tunor; Vector: puc18; Site 1: Smal;
Site 2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196, 716 - Ludwig Institute for Cancer Research)
Profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 2.1e-92;
0; Mismatches 16; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                   sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                BF769253.1 GI:12117153
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
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                                                                                                         Homo sapiens (human)
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